

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 9, 2005, 00:51:02 ; Search time 3003 Seconds
(without alignments)
1952.014 Million cell updates/sec

Title: US-09-887-194A-13
Perfect score: 154
Sequence: 1 cggcgcgagctgtcatctc.....gagatgaccagctccgccc 154

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 3966416

Minimum DB seq length: 0
Maximum DB seq length: 200

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_hic:*

4: gb_est3:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_gss1:*

9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	36.6	23.8	175	4	BF945949 CMO-NN115
2	36.6	23.8	175	4	BF945949 CMO-NN115
3	32.6	21.2	186	2	BF408161 UI-R-BJ2-
4	32.6	21.2	186	2	BF408161 UI-R-BJ2-
5	31.8	20.6	127	1	AA429110 zv78c11.r
6	31.8	20.6	127	1	AA429110 zv78c11.r
7	31.2	20.3	152	9	CL176108 104_382_1
8	31.2	20.3	152	9	CL176108 104_382_1
9	31.2	20.3	152	9	CL176109 104_382_1
10	31.2	20.3	152	9	CL176109 104_382_1
11	31	20.1	135	7	CV406622 RCO-TN007
12	31	20.1	135	7	CV406622 RCO-TN007
13	30.6	19.9	168	8	BH224923 1006122E0
14	30.6	19.9	168	8	BH224923 1006122E0
15	28.8	18.7	151	4	BI966631 id57a04.x
16	28.8	18.7	151	4	BI966631 id57a04.x
17	28.8	18.7	167	6	CA002143 HS06K10r
18	28.8	18.7	167	6	CA002143 HS06K10r
19	28.8	18.7	184	2	BF882476 CMI-ET019
20	28.8	18.7	184	2	BF882476 CMI-ET019
21	28.8	18.7	194	4	BI777398 EBrc04_SQ
22	28.8	18.7	194	4	BI777398 EBrc04_SQ
23	28.6	18.6	179	9	CE208692 tigr-gss-
24	28.6	18.6	179	9	CE208692 tigr-gss-

25	28.6	18.6	190	6	CA004311 HS17D13r
26	28.6	18.6	190	6	CA004311 HS17D13r
27	28.2	18.3	147	7	CN423515 170006000
28	28.2	18.3	147	7	CN423515 170006000
29	28.2	18.3	196	1	AI564785 tn37c01.x
30	28.2	18.3	196	1	AI564785 tn37c01.x
31	28.2	18.3	196	1	AI799725 tm80d10.x
32	28.2	18.3	196	1	AI799725 tm80d10.x
33	28.2	18.3	197	9	CL601509 OB_Ba007
34	28.2	18.3	197	9	CL601509 OB_Ba007
35	28	18.2	130	2	BF760525 RC2-CT065
36	28	18.2	130	2	BF760525 RC2-CT065
37	27.8	18.1	110	6	CB251950 3529_1_19
38	27.8	18.1	110	6	CB251950 3529_1_19
39	27.8	18.1	161	1	AI834106 606065A12
40	27.8	18.1	161	1	AI834106 606065A12
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42	27.8	18.1	163	2	BF728943 1000069F0
43	27.8	18.1	180	1	AJ469411 AJ469411
44	27.8	18.1	180	1	AJ469411 AJ469411
45	27.8	18.1	184	8	CC157563 ig24e03.b
46	27.8	18.1	184	8	CC157563 ig24e03.b
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48	27.8	18.1	196	7	D22092 RICC10326A
49	27.4	17.8	110	1	AV939923 AV939923
50	27.4	17.8	110	1	AV939923 AV939923
51	27.4	17.8	177	7	CN152194 WOUNDI_80
52	27.4	17.8	177	7	CN152194 WOUNDI_80
53	27.4	17.8	183	2	BF585740 FM1_24_A0
54	27.4	17.8	183	2	BF585740 FM1_24_A0
55	27.4	17.8	184	7	CV308094 tj49d12.b
56	27.4	17.8	184	7	CV308094 tj49d12.b
57	27.4	17.8	184	7	CV308095 tj49d12.g
58	27.4	17.8	184	7	CV308095 tj49d12.g
59	27.4	17.8	190	4	BM152340 TCBAPIE87
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61	27.4	17.8	190	8	AQ0909667 GSSTC0903
62	27.4	17.8	190	8	AQ0909667 GSSTC0903
63	27.4	17.8	198	1	AA219945 mx97f04.r
64	27.4	17.8	198	1	AA219945 mx97f04.r
65	27.2	17.7	142	5	BX603054 BX603054
66	27.2	17.7	142	5	BX603054 BX603054
67	27.2	17.7	159	9	CG480886 OST13029
68	27.2	17.7	159	9	CG480886 OST13029
69	27.2	17.7	168	1	AJ574234 AJ574234
70	27.2	17.7	168	1	AJ574234 AJ574234
71	27.2	17.7	191	6	CD607926 56044545J
72	27.2	17.7	191	6	CD607926 56044545J
73	27.2	17.7	192	6	CD607925 56044545H
74	27.2	17.7	192	6	CD607925 56044545H
75	27	17.5	194	8	BH660601 BOMPJU47TR
76	27	17.5	194	8	BH660601 BOMPJU47TR
77	26.8	17.4	100	4	BG458454 947046F05
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79	26.8	17.4	179	4	BM369834 EBem07_SQ
80	26.8	17.4	179	4	BM369834 EBem07_SQ
81	26.6	17.3	117	7	H42955 y068d06.r1
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83	26.6	17.3	147	7	CN423524 170004243
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85	26.6	17.3	171	7	CN423522 170004706
86	26.6	17.3	171	7	CN423522 170004706
87	26.6	17.3	174	7	CN297706 170005315
88	26.6	17.3	174	7	CN297706 170005315
89	26.6	17.3	180	6	C10705 WHE0945_E
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93	26.6	17.3	190	2	BE493133 WHE0567_G
94	26.6	17.3	190	2	BE493133 WHE0567_G
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96	26.6	17.3	195	6	CD962811 SDR_160 G
97	26.4	17.1	166	8	AZ983701 2M0264N24

c 98 26.4 17.1 166 8 AZ983701 2M0264N24
99 26.4 17.1 182 7 CO504865 GGEZCB100
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ALIGNMENTS

RESULT 1

BF945949

LOCUS

BF945949 175 bp mRNA linear EST 22-JAN-2001

CM0-NN1155-271000-628-a09 NN1155 Homo sapiens cDNA, mRNA sequence.

BF945949

ACCESSION

BF945949.1 GI:12363224

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

1 (bases 1 to 175)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

JOURNAL

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COMMENT

ACCESSION	UI-R-BJ2-bra-d-05-0-UI 3', mRNA sequence.
VERSION	BF408161
KEYWORDS	BF408161.1 GI:11396136
SOURCE	EST.
ORGANISM	Rattus norvegicus (Norway rat)
	Rattus norvegicus
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
	Rattus.
REFERENCE	1 (bases 1 to 186)
AUTHORS	Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE	Normalization and subtraction: two approaches to facilitate gene discovery
JOURNAL	Genome Res. 6 (9), 791-806 (1996)
MEDLINE	97044477
PUBMED	8889548
COMMENT	Contact: Soares, MB Coordinated Laboratory for Computational Genomics University of Iowa 375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA Tel: 319 335 8250 Fax: 319 335 9565 Email: bento-soares@uiowa.edu Oligo-dt track not found, Not 1 site shown in beginning of sequence is likely internal to the message. cDNA Library Preparation: M.B. Soares lab Clone distribution: clones will be available through Research Genetics (www.resgen.com) The following repetitive elements were found in this cDNA sequence: 1-21, >GC-rich#Low complexity Seq_primer: M13 Forward POLYA=No.

FEATURES	Location/Qualifiers
SOURCE	1. .186

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1. .186
/organism="Rattus norvegicus"
/mol_type="mRNA"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-BJ2-bra-d-05-0-UI"
/lab_host="DH10B (Life Technologies)"
/clone_lib="UI-R-BJ2"
/notes="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-BJ2
library is a subtracted library derived from the following
tissues: heart, atrium at 15 dpc, ventricle at 16.5 dpc,
atrium at 16.5 dpc, ventricle at 13 dpc, ventricle at 15
dpc, AV canal at 15 dpc. For a detailed description of
the library from which this clone was derived, please
visit our web site at ratec.eng.uiowa.edu. The
subtraction has been previously described in (Bonaldo,
Lemon and Soares, Genome Research 6:791-806, 1996)
TAG SEQ=None found"

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ORIGIN

Query Match	21.2%	Score 32.6;	DB 2;	Length 186;
Best Local Similarity	54.6%;	Pred. No. 3.2e+02;		
Matches 65; Conservative	0;	Mismatches 54;	Indels 0;	Gaps 0;

[illegible]

RESULT 4	186 bp	mRNA	linear	EST 28-NOV-2000
BF408161/c				
LOCUS	BF408161			
DEFINITION	UI-R-BJ2-bra-d-05-0-UI.s1 UI-R-BJ2 Rattus norvegicus CDNA clone			
ACCESSION	UI-R-BJ2-bra-d-05-0-UI 3', mRNA sequence.			
VERSION	BF408161			
	BF408161.1	GI:11396136		

KEYWORDS	EST.
SOURCE	Rattus norvegicus (Norway rat)
ORGANISM	Rattus norvegicus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE	1 (bases 1 to 186)
AUTHORS	Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE	Normalization and subtraction: two approaches to facilitate gene discovery
JOURNAL	Genome Res. 6 (9), 791-806 (1996)
MEDLINE	97044477
PUBMED	8889548
COMMENT	Contact: Soares, MB

Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road , 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@uiowa.edu
Oligo-dt track not found, Not I site shown in beginning of sequence
is likely internal to the message. cDNA Library Preparation: M.B.
Soares lab Clone distribution: clones will be available through
Research Genetics (www.resgen.com) The following repetitive
elements were found in this cDNA sequence: 1-21,
>GC_rich#Low_complexity
Seq_primer: M13 Forward
POLYA=No.

FEATURES

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Location/Qualifiers
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/mol_type="mRNA"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
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/lab_host="DH10B (Life Technologies)"
/clone_1lb="UI-R-BJ2"
/clone_2lb="UI-R-BJ2"
/notes="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-BJ2
library is a subtracted library derived from the following
tissues: heart, atrium at 15 dpc, ventricle at 16.5 dpc,
atrium at 16.5 dpc, ventricle at 13 dpc, ventricle at 15
dpc, AV canal at 15 dpc. For a detailed description of
the library from which this clone was derived, please
visit our web site at ratest.eng.uiowa.edu. The
subtraction has been previously described in (Bonaldo,
Lennon and Soares, Genome Research 6:791-806, 1996)
TAG SEQ=None found"

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ORIGIN

Query Match	21.24;	Score 32.6;	DB 2;	Length 186;
Best Local Similarity	54.6%;	Pred. No. 3.2e+02;		
Matches 65; Conservative	0;	Mismatches 54;	Indels 0;	Gaps 0;

[illegible]

RESULT 5	AA429110	127 bp	mRNA	linear	EST 16-OCT-1997
LOCUS	AA429110				
DEFINITION	zv78c11.r1 Soares total_fetus_Nb2HP8_9w Homo sapiens cDNA clone IMAGE:759764 5' similar to TR:G307309 G307309 HISTONE H4. [1] ;,				
	mRNA sequence.				
ACCESSION	AA429110				
VERSION	AA429110.1	GI:2110653			
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				

ORIGIN

REFERENCE 1 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 135)
AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bata, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. <http://www.ludwig.org.br>.
location/Qualifiers
1. 135
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="TN0078"
/note="Organ: testis normal; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORSTBS PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
ORIGIN
Query Match 20.1%; Score 31; DB 7; Length 135;
Best Local Similarity 62.0%; Pred. No. 8.1e+02;
Matches 49; Conservative 0; Mismatches 30; Indels 0; Gaps 0;
QY 76 GGCCGCCGACTGACGATGAGCGAGATGACCGCTCCGCCCGCGACTCGACGATGACG 135
DB 135 GGTCGTAGTCTGGTGTGAGGGAAGACACGTCGGCGCGTAGCGTGGTGTGAGGG 76
QY 136 AGATGACCACTCCGCGCG 154
DB 75 AAAGTACCACGTCGGCGG 57
RESULT 13
BH224923 168 bp DNA linear GSS 08-NOV-2001
LOCUS 1006122E07.2EL_xl 1006 - RescueMu Grid G Zea mays genomic, genomic
DEFINITION survey sequence.
ACCESSION BH224923
VERSION BH224923.1 GI:16822338
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 168)
AUTHORS Walbot, V.
TITLE Maize genomic sequences found using engineered RescueMu transposon
JOURNAL Unpublished (2001)
COMMENT Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA

Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Plate: 1006122 column: 15
Class: transposon-tagged.
location/Qualifiers
1. 168
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="1006 - RescueMu Grid G"
/note="Organ: leaf; Vector: RescueMu (engineered from Bluescript backbone); Site 1: BamHI; Site 2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'www.zmdb.iastate.edu' and follow the links for 'RescueMu.' Grid G was grown at Stanford in 2000. DNA was extracted from leaf punches, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."
ORIGIN
Query Match 19.9%; Score 30.6; DB 8; Length 168;
Best Local Similarity 60.0%; Pred. No. 1e+03;
Matches 51; Conservative 0; Mismatches 34; Indels 0; Gaps 0;
QY 49 GGTCACTCGCTCATCGTCGAGTCGGCGCGCGCGCGACTCGACGATGACGACG 108
DB 33 GGGCTTCACGCTCCGCGTCGGCCAGGTGGCGCGCGCTCGCTCCGCAAGGACGCGTCCG 92
QY 109 CTCCGGCGCGCGACTCGACGATGAG 133
DB 93 CGTCGCCGTGAGCCCGACGAGAG 117
RESULT 14
BH224923 168 bp DNA linear GSS 08-NOV-2001
LOCUS 1006122E07.2EL_xl 1006 - RescueMu Grid G Zea mays genomic, genomic
DEFINITION survey sequence.
ACCESSION BH224923
VERSION BH224923.1 GI:16822338
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 168)
AUTHORS Walbot, V.
TITLE Maize genomic sequences found using engineered RescueMu transposon
JOURNAL Unpublished (2001)
COMMENT Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Plate: 1006122 column: 15
Class: transposon-tagged.
location/Qualifiers
FEATURES

source 1.168
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="1006 - Rescuemu Grid G"
/note="Organ: leaf; Vector: Rescuemu (engineered from pBluescript backbone); Site 1: BamHI; Site 2: BglII; Rescuemu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on Rescuemu, go to the web site 'www.zmdb.iastate.edu' and follow the links for 'Rescuemu.' Grid G was grown at Stanford in 2000. DNA was extracted from leaf punches, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

Query Match 19.9%; Score 30.6; DB 8; Length 168;
Best Local Similarity 60.0%; Pred. No. 1e+03;
Matches 51; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

Qy 22 CTCATCGTCGAGTCGGCGCGGAGCTGTCATCTCGCTCATCTGAGTCGGCGCGCCG 81
Db 117 CTCCTCGTCGGGCTCGACGCGCGAGCGCGAGCGCTCCCTGGCGAGCGCGCGCCAC 58
Qy 82 CGACTCGACGATGACGAGATGACC 106
Db 57 CTGGCCGACGCGAGCGTGAGCCC 33

RESULT 15
BI966631 151 bp mRNA linear EST 12-MAR-2002
LOCUS id57a04.x1 Melton Normalized Mixed Mouse Pancreas 1 N1-MMS1 Mus
DEFINITION musculus cDNA clone IMAGE:5666983 3' similar to TR:P94852 P94852
PII PROTEIN.; mRNA sequence.

ACCESSION BI966631 GI:16341036
VERSION BI966631
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K., Lemishka, I., Scarce, M., Brestelli, J., Gradwohl, G., Clifton, S., Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blistain, A., Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagareishvili, R., Williams, T., Jackson, Y. and Bowers, Y.
TITL
JOURN
COMMENT Endocrine Pancreas Consortium
Unpublished (2000)
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge, MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. Douglas Melton DNA sequencing by: Washington University Genome Sequencing Center For information on obtaining a clone please contact: Juliana Brown (brown@fas.harvard.edu)
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
MGI:1953309 This sequence now available from the IMAGE consortium,

for clone orders contact: info@image.llnl.gov
High quality sequence stop: 1.
Location/Qualifiers
1.151
source

/organism="Mus musculus"
/mol_type="mRNA"
/strain="ICR"
/db_xref="taxon:10090"
/clone="IMAGE:5666983"
/sex="Both for embryonic & newborn, male for adult and adult islet"
/dev_stage="Embryonic day 10.5, E12.5, E16.5, newborn, adult, mixed"
/lab_host="DH10B"
/clone_lib="Melton Normalized Mixed Mouse Pancreas 1 N1-MMS1"
/note="Vector: pSPORT1; Site 1: Not I; Site 2: Sal I; Five libraries representing E10.5/12.5 pancreatic bud, E16.5 pancreas, newborn pancreas, adult pancreas, and adult islets of Langerhans were separately constructed using SuperScript Plasmid Library kit (Life Technologies). cDNA was made by oligo-dT priming and size-selected by column fractionation. Libraries were amplified once on solid support and plasmid DNA from each library was prepared and mixed in equal amounts. The mixed library DNA was normalized by method #4 from Bonaldo, Lennon, and Soares 1996 Genome Research 6:791-806; 0.5 microgram single-stranded mixed library plasmid DNA was mixed with 5 micrograms PCR product representing mixed library inserts and hybridized to an EcoT of 6. Single-stranded (unhybridized) plasmids were isolated by hydroxyapatite chromatography and used to make this library."

Query Match 18.7%; Score 28.8; DB 4; Length 151;
Best Local Similarity 60.0%; Pred. No. 2.8e+03;
Matches 48; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

Qy 40 GCCGAGCTGTCATCTCGCTCATCTGAGTCGGCGCGCCGCGACTCGACGATGACCGA 99
Db 34 GCTCGAGAGGTCCGCGAGGCTTCGCCGAGGTGGCGCTCACCGGCTGACCGTACCGA 93
Qy 100 GATGACGAGCTCCGCGCGCC 119
Db 94 GGTCAAGGCTTCGCGCCGCC 113

RESULT 16
BI966631/c 151 bp mRNA linear EST 12-MAR-2002
LOCUS id57a04.x1 Melton Normalized Mixed Mouse Pancreas 1 N1-MMS1 Mus
DEFINITION musculus cDNA clone IMAGE:5666983 3' similar to TR:P94852 P94852
PII PROTEIN.; mRNA sequence.

ACCESSION BI966631 GI:16341036
VERSION BI966631
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K., Lemishka, I., Scarce, M., Brestelli, J., Gradwohl, G., Clifton, S., Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blistain, A., Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagareishvili, R., Williams, T., Jackson, Y. and Bowers, Y.
TITL
JOURN
COMMENT Endocrine Pancreas Consortium
Unpublished (2000)
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,

Email: stein@ipk-gatersleben.de
Insert Length: 167 Std Error: 0.00
Plate: 6 row: K column: 10
Seq primer: M13rev.

FEATURES
source

1.167
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/cultivar="barke"
/sub_species="vulgare"
/db_xref="GABI:257345"
/db_xref="taxon:112509"
/clone="HS06K10"
/tissue_type="embryo + scutellum"
/dev_stage="0-16 hours after imbibition"
/lab_host="XL10-Gold"
/clone_lib="HS"
/note="Vector: pBluescript SK+, Site 1: EcoRI (5'-end of cDNA); Site 2: XhoI (3'-end of cDNA); Due to a cloning artefact caused by the kit, in most cases the EcoRI site is NOT present, as well as the EcoRI adapter used for cloning. To excise the insert, restriction sites upstream EcoRI should be used (e.g. BamHI, SalI, PstI). NOTE: Also due to the cloning system used Blue/white selection for recombinants is not 100% reliable."

ORIGIN

Query Match 18.7%; Score 28.8; DB 6; Length 167;
Best Local Similarity 56.2%; Pred. No. 2.8e+03;
Matches 54; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

OY 4 CCGAGCTGTCATCTCTCATCTGTCAGTCGGCGCCGAGCTGTCTCTCAT 63
|||
DB 130 CCGCTCCGCTCTTCTCCAGCTGTCGCCCGCGATCTGACGGCCCTCGGCATCTTCTCAC 71
|||
OY 64 CGTCGAGTCGGCGCGCCGCGACTCGACGATGAGCGA 99
|||
DB 70 CTCGGCGCGCGCGCGCGCAGCGAGAGCGCCGA 35
|||

RESULT 19
BF882476 184 bp mRNA linear EST 17-JAN-2001
LOCUS BF882476
DEFINITION CM1-ET0191-051200-626-b02 ET0191 Homo sapiens cDNA, mRNA sequence.
ACCESSION BF882476
VERSION BF882476.1 GI:12272602
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS
1 (bases 1 to 184)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
JOURNAL MEDLINE
PUBMED
COMMENT
TITLE
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM1&t2=CM1-ET0191-051200-626-b02&t3=2000-12-05&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 24
High quality sequence stop: 180.

FEATURES
source

1.184
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="ET0191"
/note="Organ: lung tumor; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Query Match 18.7%; Score 28.8; DB 2; Length 184;
Best Local Similarity 65.6%; Pred. No. 2.8e+03;
Matches 42; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

OY 91 GATGAGCGAGATGACCACTCCGCGCCGCGCTCGACGATGAGCGAGATGACCAGCTCCG 150
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DB 103 GGTGAGGGAAGACCACTCGGGCGGTAGCTGGGTGTGAGGGAAGACCACTCCG 162
|||
OY 151 GCCG 154
|||
DB 163 GCCG 166
|||

RESULT 20
BF882476 184 bp mRNA linear EST 17-JAN-2001
LOCUS BF882476
DEFINITION CM1-ET0191-051200-626-b02 ET0191 Homo sapiens cDNA, mRNA sequence.
ACCESSION BF882476
VERSION BF882476.1 GI:12272602
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS
1 (bases 1 to 184)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
JOURNAL MEDLINE
PUBMED
COMMENT
TITLE
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM1&t2=CM1-ET0191-051200-626-b02&t3=2000-12-05&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 24
High quality sequence stop: 180.
Location/Qualifiers

FEATURES

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source
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        /db_xref="taxon:9606"
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        /note="Organ: lung tumor; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Query Match      18.7%; Score 28.8; DB 2; Length 184;
Best Local Similarity 65.6%; Pred. No. 2.8e+03;
Matches 42; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

Oy      1 CGGCGGAGCTGTGCATCTTCCTCATCGTGCAGTCGGCGCCGAGCTGTCATCTGCT 60
         ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      166 CCGCCCCGACGTGTCTTTCCCTCACCACCAGCCTACCGCCGATGTGTCTTCCCT 107

Oy      61 CATC 64
         |||
Db      106 CACC 103

RESULT 21
LOCUS      BI777398          194 bp      mRNA       linear     EST 23-JUL-2002
DEFINITION EBR004_SQ001_B16_R root, 3 week, salt-stressed, cv Optic, EBR004
            Hordeum vulgare subsp. vulgare cDNA clone EBR004_SQ001_B16 5', mRNA
            sequence.
KEYWORDS   BI777398
SOURCE     BI777398.2 GI:21948919
ORGANISM   Hordeum vulgare subsp. vulgare
            Hordeum vulgare subsp. vulgare
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Pooideae; Triticeae; Hordeum.
REFERENCE  1 (bases 1 to 194)
            Hedley,P., Liu,H., Caldwell,D., McCallum,N., Mudie,S., Cardle,L.,
            Ramsay,L., Machray,G., Marshall,D.F.M. and Waugh,R.
            Development of Barley Transcriptome Resources
            Unpublished (2001)
            On Sep 26, 2001 this sequence version replaced gi:15780290.
            Contact: Waugh R, Marshall DF
            Genome Dynamics/Computational Biology
            Scottish Crop Research Institute
            Invergowrie, Dundee, DD2 5DA, Scotland, UK
            Tel: 00 44 1382 562731
            Fax: 00 44 1382 562426
            Email: est@scrl.sarl.ac.uk
            All sequence has a phred quality score of 20 or over
            Seq primer: M13 reverse.

FEATURES             Location/Qualifiers
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                     /sub_species="vulgare"
                     /db_xref="taxon:112509"
                     /clone="EBR004 SQ001_B16"
                     /tissue_type="root"
                     /dev_stage="3 week"
                     /lab_host="DH10B"
                     /clone_1lb="root, 3 week, salt-stressed, cv Optic, EBR004"
                     /note="Vector: pSPORT1; Site 1: Sal I; Site 2: Not I;
                     Non-normalised library, directionally cloned into pSPORT1.
                     Derived from roots of 3 week old salt stressed barley
                     plants. Developed as part of the barley transcriptome

```

[illegible]

QY 10 CTGTCATCTCGCTCATCTGTCAGTCGGCGCCGGAGCTGTCATCTCGCTCATCTGTCGA 69
 188 CCGGCCCGTGCACTCTCCGTGAAGCCGCAGCACTGCACGCGCACTTCATCCAACTCTTC 129
 QY 70 GTCGGCGCCGCCGACTGACGATGAGCGAGATGACCAGCTCCGCGCCGCACTCGACGA 129
 128 GCGCGCTTGCACTCCGCCCTTCATGTGTCAAGACCTCCAAGTCAAGACCTCTATCGCCGC 69
 QY 130 TGAGCGAGATGACCAAGCTCCGACC 153
 68 CGAGAAAGAAAAACCCGCGCGCTTC 45
 Db

RESULT	23			
CE208692				
LOCUS		179 bp	DNA	
DEFINITION	CE208692		linear	GSS 25-SEP-2003
	tigr-gss-dog-17000372681097	Dog	Library	Canis familiaris genomic,
	genomic survey sequence.			

SOURCE ORGANISM	REFERENCE
<i>Canis familiaris</i> (dog)	Kirkness, E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K.
<i>Canis familiaris</i>	1 (bases 1 to 179)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.	

TITLE The dog genome: survey sequencing and comparative analysis
 JOURNAL Science 301 (5641), 1898-1903 (2003)
 MEDLINE 22875432
 PUBMED 14512627
 COMMENT
 Contact: Kirkness EF
 The Institute for Genomic Research
 Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
 Rockville, MD 20850, USA
 Tel: 301-838-0200
 Fax: 301-838-0208
 Email: ekirkness@tigr.org
 Class: shotgun.

```

FEATURES
source
Location/Qualifiers
1. .179
/organism="Canis familiaris"
/mol_type="genomic DNA"
/strain="Standard Poodle"
/db_xref="taxon:9615"
/clone_lib="Dog Library"
/note="Site 1: BstXI; Libraries were prepared from
peripheral blood"

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RESULT	24
CE208692/c	
LOCUS	
DEFINITION	tigr-gss-dog-17000372681097 Dog Library Canis familiaris genomic,
	genomic survey sequence.
ACCESSION	CE208692
VERSION	CE208692.1 GI:35364347

KEYWORDS	GSS.
SOURCE	Canis familiaris (dog)
ORGANISM	Canis familiaris Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE	1 (bases 1 to 179)
AUTHORS	Kirtness, E.F., Batina, V., Halpern, A.L., Levy, S., Remington, K.,

COMMENT:
Contact: Kirkness EF
The Institute for Genomic Research
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Tel: 301-838-0200
Fax: 301-838-0208
Email: ekirkness@tigr.org
Class: shotgun.

```

FEATURES
source
Location/Qualifiers
1. .179
/organism="Canis familiaris"
/mol_type="genomic DNA"
/strain="Standard Poodle"
/db_xref="taxon:9615"
/clone_lib="Dog Library"
/note="Site 1: BstXI; Libraries were prepared from
peripheral blood"

```

RESULT 25	CA004311	LOCUS	DEFINITION
CA004311	190 bp	HS Hordeum vulgare subsp. vulgare	EST 23-OCT-2002
HS17D13r		5-PRIME, mRNA sequence.	cdna clone HS17D13

Molecular Markers Group, Department Genbank
Institute of Plant Genetics and Crop Plant Research (IPK)
Corrensstr. 3, 06466, Gatersleben, Germany
Tel: 039482-5522
Fax: 039482-5595
Email: stein@ipk-gatersleben.de
Insert Length: 190 Std Error: 0.00
Plate: 17 row: D column: 13
Seq primer: M13rev.

QY 97 CGAGATGACCAGTCCGGCCCGGACTCG 125
| | | | | | | | | | | | | | | | | |
Db 96 CTACGTCCCGAGCTCCAGCCGGGCTCG 124

RESULT 28
CN423515/c 147 bp mRNA linear EST 16-MAY-2004
LOCUS 1700600057518 GRN_PREHEP Homo sapiens cDNA 5', mRNA sequence.
ACCESSION CN423515
VERSION CN423515.1 GI:47411109
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J.,
Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R.,
Lebkowski, J and Stanton, L.W.
TITLE Transcriptome characterization elucidates signaling networks that
control human ES cell growth and differentiation
JOURNAL Nat. Biotechnol. 22 (6), 707-716 (2004)
COMMENT Contact: Brandenberger R
Regenerative Medicine
Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert Length: 147 Std Error: 0.00.
Location/Qualifiers
1. 147
/organism="Homo sapiens"
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/issue_type="embryonic stem cells, DMSO-treated H9 cell
line"
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/note="oligo dt primed, full-length enriched cDNA library
from DMSO-treated hES cell line H9 (p22) maintained in
feeder-free conditions"

ORIGIN
Query Match 18.3%; Score 28.2; DB 7; Length 147;
Best Local Similarity 57.3%; Pred. No. 4e+03;
Matches 51; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

QY 30 CGAGTCGGCGCGCCGAGCTGTCATCTCGTCATCTGAGTCGGCGCCGCACTCGA 89
| | | | | | | | | | | | | | | | | |
Db 124 CGAGCCGGCGGCTGAGCTGGGACGTAGACCTAGTGCAGCCGAGCGAAGAAATCC 65

QY 90 CGATGAGCGAGATGACCAGCTCCGGCCGC 118
| | | | | | | | | | | | | | | | | |
Db 64 CGCCGAACGCGAGACACCGCCGCCGACG 36

RESULT 29
AI564785 196 bp mRNA linear EST 12-MAY-1999
LOCUS tn37c01.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2169792 3',
DEFINITION mRNA sequence.
ACCESSION AI564785
VERSION AI564785.1 GI:4523242
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS NCI/NINDS-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE NCI/NINDS-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute / National Institute of Neurological

JOURNAL
COMMENT Disorders and Stroke, Brain Tumor Genome Anatomy Project
(CGAP/BTGAP), Tumor Gene Index
Unpublished (1998)
Contact: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/ILNI at:
www-bio.lnl.gov/bbrp/image/image.html
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POLYA=NO.

FEATURES
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/db_xref="taxon:9606"
/clone="IMAGE:2169792"
/tissue_type="anaplastic oligodendroglioma"
/lab_host="DH10B"
/clone_lib="NCI CGAP Brn25"
/note="Organ: brain; Vector: pT7T3D-Pac (Pharmacia) with a
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dt) primer [5'
TGTTACCAATCTGAAGTGGAGCGCGGCATAGTTTCTTTTCTTTTCTTTT
T 3']; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT7T3 vector.
Library is normalized, and was constructed by Bento
Soares and M.Fatima Bonaldo."

ORIGIN
Query Match 18.3%; Score 28.2; DB 1; Length 196;
Best Local Similarity 57.3%; Pred. No. 4e+03;
Matches 51; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

QY 30 CGAGTCGGCGCGCCGAGCTGTCATCTCGTCATCTGAGTCGGCGCCGCACTCGA 89
| | | | | | | | | | | | | | | | | |
Db 104 CGAGCCGGCGGCTGAGCTGGGACGTAGACCTAGTGCAGCCGAGCGAAGAAATCC 163

QY 90 CGATGAGCGAGATGACCAGCTCCGGCCGC 118
| | | | | | | | | | | | | | | | | |
Db 164 CGCCGAACGCGAGACACCGCCGCCGACG 192

RESULT 30
AI564785 196 bp mRNA linear EST 12-MAY-1999
LOCUS tn37c01.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2169792 3',
DEFINITION mRNA sequence.
ACCESSION AI564785
VERSION AI564785.1 GI:4523242
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS NCI/NINDS-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE NCI/NINDS-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute / National Institute of Neurological
Disorders and Stroke, Brain Tumor Genome Anatomy Project
(CGAP/BTGAP), Tumor Gene Index
Unpublished (1998)
Contact: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima

RESULT 35
LOCUS BF760525 130 bp mRNA linear EST 12-JAN-2001
DEFINITION RC2-CT0652-211200-011-b01 CT0652 Homo sapiens cDNA, mRNA sequence.
ACCESSION BF760525
VERSION BF760525.1 GI:12108425
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?cl=RC2&t2=RC2-CT0652-211200-011-b01&t3=2000-12-21&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 23
High quality sequence stop: 130.
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1. .130
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="CT0652"
/note="Organ: colon; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
ORIGIN
Query Match 18.2%; Score 28; DB 2; Length 130;
Best Local Similarity 63.2%; Pred. No. 4.5e+03;
Matches 43; Conservative 0; Mismatches 25; Indels 0; Gaps 0;
QY 85 CTCGACGATGACGACGATGACGATCCGCGCCGCGACTGACGATGACGACGATGACCA 144
DB 24 CTGGGTGTGACGGGAAGACCAACGTTGGCGGTATGCTGCGGTGTGAGAGAATGACCA 83
QY 145 GCTCCGGC 152
DB 84 CGTCGGGC 91
RESULT 36
LOCUS BF760525 130 bp mRNA linear EST 12-JAN-2001
DEFINITION RC2-CT0652-211200-011-b01 CT0652 Homo sapiens cDNA, mRNA sequence.
ACCESSION BF760525
VERSION BF760525.1 GI:12108425

KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?cl=RC2&t2=RC2-CT0652-211200-011-b01&t3=2000-12-21&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 23
High quality sequence stop: 130.
FEATURES
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1. .130
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="CT0652"
/note="Organ: colon; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
ORIGIN
Query Match 18.2%; Score 28; DB 2; Length 130;
Best Local Similarity 63.2%; Pred. No. 4.5e+03;
Matches 43; Conservative 0; Mismatches 25; Indels 0; Gaps 0;
QY 3 GCCGAGCTGTCATCTGCTCATCTGTCGATCGCGCGCGAGCTGTCATCTGCTCA 62
DB 91 GCCCGAGTGTGTCATTCTTCTACACCAACGATACCGCCCAACGTGCTTCCCTCA 32
QY 63 TCGTCGAG 70
DB 31 CCACCCAG 24
RESULT 37
LOCUS CB251950 110 bp mRNA linear EST 19-FEB-2003
DEFINITION 3529_1_19_1_H10_Y_1 3529 - 2 mm ear tissue from Schmidt and Hake
ACCESSION CB251950
VERSION CB251950.1 GI:28422637
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

Db 66 CTGTCATGTCGGTCTTACGTAAGCCCGGGTGGCGGAGTTGACGGCAGCTCGGGGTGC 125

Qy 107 AGCTCGGGCCCGGACTCGACGATGAG 133

Db 126 CGCCTCGCCAGACCCCTCGAGTAGAG 152

RESULT 40

AI834106/c 161 bp mRNA linear EST 02-FEB-2000

LOCUS 606065A12.x1 606 - Ear tissue cDNA library from Schmidt lab Zea

DEFINITION mays cDNA, mRNA sequence.

ACCESSION AI834106

VERSION AI834106.1 GI:5456416

KEYWORDS EST.

SOURCE Zea mays

ORGANISM Zea mays

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

AUTHORS 1 (bases 1 to 161)

TITLE Walbot, V.

REFERENCE 1 (bases 1 to 161)

AUTHORS Maize ESTs from various cDNA libraries sequenced at Stanford University

TITLE Unpublished (1999)

JOURNAL Contact: Walbot V

COMMENT Department of Biological Sciences

Stanford University

855 California Ave, Palo Alto, CA 94304, USA

Tel: 650 723 2227

Fax: 650 725 8221

Email: walbot@stanford.edu

Plate: 606065 row: A column: 12.

LOCATION/Qualifiers

1. .161

/organism="Zea mays"

/mol_type="mRNA"

/cultivar="Ohio43"

/db_xref="taxon:4577"

/tissue_type="mixed"

/dev_stage="ear length from 0.5 cm - 2.0 cm"

/lab_host="XLOLR (Stratagene)"

/clone_lib="606 - Ear tissue cDNA library from Schmidt lab"

/note="Organ: immature ear; Vector: pBK-CMV; Site_1: EcorI; Site_2: XhoI; Mixed ear tissue cDNA library from Schmidt lab"

ORIGIN

Query Match 18.1%; Score 27.8; DB 1; Length 161;

Best Local Similarity 57.5%; Pred. No. 5e+03;

Matches 50; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

Qy 22 CTCACTCGATCGAGTCGGCGCGGAGCTGTCACTTCGCTCATCTCGAGTCGGCGCGCC 81

Db 152 CTCTACTCGAGGGTCTCTGGCGAGCGGCACCCCGAGCTGCGCTCACTGCGCGCACCC 93

Qy 82 CGACTCGACGATGAGCGAGATGACCAAG 108

Db 92 GGGCTACGTGAAGACCGACATGACCAG 66

RESULT 41

BF728943 163 bp mRNA linear EST 09-JAN-2001

LOCUS 1000069F04.x2 1000 - Unigene I from Maize Genome Project Zea mays

DEFINITION cDNA, mRNA sequence.

ACCESSION BF728943

VERSION BF728943.1 GI:12046804

KEYWORDS EST.

SOURCE Zea mays

ORGANISM Zea mays

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

AUTHORS 1 (bases 1 to 163)

TITLE Walbot, V.

REFERENCE Maize ESTs from various cDNA libraries sequenced at Stanford University

JOURNAL Unpublished (1999)

COMMENT Contact: Walbot V

Department of Biological Sciences

Stanford University

855 California Ave, Palo Alto, CA 94304, USA

Tel: 650 723 2227

Fax: 650 725 8221

Email: walbot@stanford.edu

Plate: 100069 row: F column: 04.

LOCATION/Qualifiers

1. .163

/organism="Zea mays"

/mol_type="mRNA"

/db_xref="dbEST:945002F06.X3"

/db_xref="taxon:4577"

/clone_lib="1000 - Unigene I from Maize Genome Project"

/note="This library represents the unique ESTs found in the first round of EST sequencing at Stanford University for the maize genome project. Sequences are present from libraries 486, 487, 496, 603, 605, 606, 614, 618, 660, 683, 687, 707, and 945. Contigs were assembled using TIGR's CAP program and a representative EST from each contig was selected for the Unigene set. All singlets were also selected."

ORIGIN

Query Match 18.1%; Score 27.8; DB 2; Length 163;

Best Local Similarity 62.0%; Pred. No. 5e+03;

Matches 44; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

Qy 49 GGTCACTCGCTCATGTCGAGTCGGCGCGCGGACTCGACGATGAGCGAGATGACCAG 108

Db 65 GCTCACCTCGCGCGCGCTCAAGCCCGACGCGGCTACTACACGCTGAGCGCAGATCAAGG 124

Qy 109 CTCCGCGCGCC 119

Db 125 CGCCATCCGGC 135

RESULT 42

BF728943/c 163 bp mRNA linear EST 09-JAN-2001

LOCUS 1000069F04.x2 1000 - Unigene I from Maize Genome Project Zea mays

DEFINITION cDNA, mRNA sequence.

ACCESSION BF728943

VERSION BF728943.1 GI:12046804

KEYWORDS EST.

SOURCE Zea mays

ORGANISM Zea mays

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

AUTHORS 1 (bases 1 to 163)

TITLE Walbot, V.

REFERENCE Maize ESTs from various cDNA libraries sequenced at Stanford University

JOURNAL Unpublished (1999)

COMMENT Contact: Walbot V

Department of Biological Sciences

Stanford University

855 California Ave, Palo Alto, CA 94304, USA

Tel: 650 723 2227

Fax: 650 725 8221

Email: walbot@stanford.edu

Plate: 100069 row: F column: 04.

LOCATION/Qualifiers

1. .163


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/organisms="Zea mays"
/mol_type="mRNA"
/db_xref="dbEST:945002F06.X3"
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/clone_lib="1000 - Unigene I from Maize Genome Project"
/note="This library represents the unique ESTs found in
the first round of EST sequencing at Stanford University
for the maize genome project. Sequences are present from
libraries 486, 487, 496, 603, 605, 606, 614, 618, 660,
683, 687, 707, and 945. Contigs were assembled using
TIGR's CAP program and a representative EST from each
contig was selected for the Unigene set. All singlets were
also selected."

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ORIGIN

Query Match	18.1%;	Score 27.8;	DB 2;	Length 163;
Best Local Similarity	62.0%;	Pred. No. 5e+03;		
Matches 44;	Conservative	0;	Mismatches 27;	Indels 0;
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Oy 36 GCGCGCCGAGCTGTATCTCGCTCATCTGAGTCGCGCGCGCGGCGGACTCGACGATGA 95
 Db 135 GCGCGATGCGCGCCCTTATCTGCTCAGCGTGTAGTACCGCGCGCTGACGCGG 76

QY	96	CGGAGTGACC	106
Db	75	CGGAGGTGAGC	65

RESULT 43

AJ469411	180 bp	mRNA	linear	EST 24-MAY-2002
LOCUS	AJ469411			
DEFINITION	S00008 Hordeum vulgare	CDNA clone	S0000800047F11F1,	mRNA

ACCESSION	AJ469411	
VERSION	AJ469411.1	GI:21185367
KEYWORDS	EST	

ORGANISM	SOURCE
Hordeum vulgare	Hordeum vulgare
Hordeum vulgare	Hordeum vulgare
Eutaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;	
Poaceae; Triticeae; Hordeum.	

REFERENCE 1 (bases 1 to 180)
AUTHORS Saren, A.-M., Tanskanen, J., Paulin, L. and Schulman, A.H.

TITLE	Barley EST's
JOURNAL	Unpublished (2002)
COMMENT	Contact: Schulman AH

University of Helsinki
P.O.Box 56 (Vikinkaaari 6A), University of Helsinki FIN-00014
Finland.

FEATURES

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1. 180
/organism="Hordeum vulgare"
/mol_type="mRNA"
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ORIGIN

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Best Local Similarity	57.5%;	Pred. No. 5e+03;		
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			Indels	0;
			Gaps	0;

Qy 46 GCTGTCATCTCGCTCATCGTCGAGTCGCGCGCCGCGACTCGACGATGAGCGAGATGAC 105
 24 GCGGCGGACGCGCGCGCGCGCGGAGGAGGAGGAGCGACGCGCATCACCATCAAGGCGCTCG 83
 Db

106 CAGCTCCGGCGCCGACTCGACGATGA 132

Db 84 CATCTCCGGCCGGCCTCTACCTGA 110

RESULT	44
AJ469411/c	
LOCUS	AJ469411
DEFINITION	S00008 Hordeum vulgare cdna clone S0000800047F11F1, mRNA
	180 bp
	mRNA
	linear
	EST 24-MAY-2002

ACCESSION	AJ469411	
VERSION	AJ469411.1	GI:21185367
KEYWORDS	EST.	
SOURCE	Hordeum vulgare	
ORGANISM	Hordeum vulgare	

Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Hordeum.

REFERENCE
1 (bases 1 to 180)
Søren A.-M., Tanskanen, J., Paulin, L. and Schulman, A. H.
ATPOPS

TITLE	Barley Est. s
JOURNAL	unpublished (2002)
COMMENT	Contact: Schulman AH

Institute of Biotechnology
University of Helsinki
P.O.Box 56 (Vilkkinkaa 6A), University of Helsinki FIN-00014,
Finland.

FEATURES

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1.  /organism="Hordeum vulgare"
2.  /mol_type="mRNA"
3.  /db_xref="taxon:4513"
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ORIGIN

Query Match	18.1%	Score 27.8;	DB 1;	Length 180;
Best Local Similarity	57.5%;	Pred. No. 5e+03;		
Matches 50; Conservative	0;	Mismatches 37;	Indels 0;	Gaps 0;

QY 23 TCATCGTAGTGGGCGCCGGAGCTGTCACTGCCTCATGTCGAGTCGGCGGCCGC 82
 ||| |||| | ||||||| | | | | | | | | | |
Db 110 TCCAGTAGAGCGGCGCCGGAGATGCGCAGCCCTTGATGTGTGATGGCGTCTCTCC 51

QY 83 GACTCGACGATGAGCGAGATGACCAGC 109
||| | | | | | | | |
Db 50 TCCTCCGCGCCGGGGCGTCCGCCGC 24

RESULT 45

	184 bp	DNA linear	GSS 29-APR-2003
CC157563			
LOCUS	CC157563		
DEFINITION	ig24e03.b1 WGS-ZmaysF (DH5a methyl)	filtered	Zea mays genomic clone
	ig24e03, genomic survey sequence.		

ACCESSION	CC157563
VERSION	CC157563.1
	GI:30182343

KEYWORDS

SOURCE
ORGANISM

ORGANISM *Zea mays*
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
: Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
Clade: Panicoideae; Andropogoneae; Zea.

REFERENCE
1 (bases 1 to 184)
Rabinowicz, P.D., O'Shaughnessy, A.L., Balija, V., Dedhia, N.,
AUTHORS
Nascimento, L.

TITLE	Genomic shotgun sequences from Zea mays (methyl-filtered)
JOURNAL	Unpublished (2002)
COMMENT	Contact: W. Richard McCombie

COMMENT
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA

Tel: 516 367 8884
Fax: 516 367 8874
Email: mccombie@cshl.org

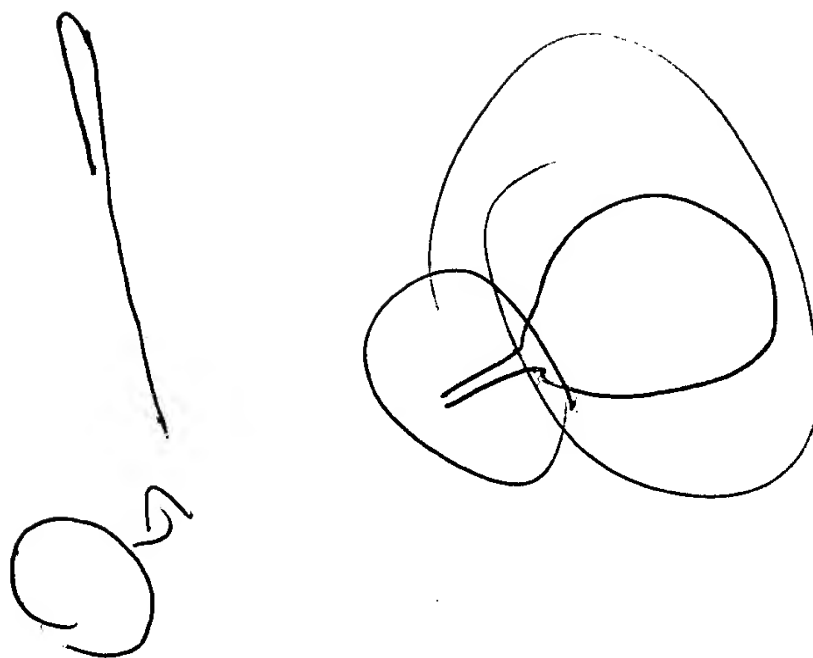
Plate: ig24 row: e column: 03
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Class: shotgun
High quality sequence stop: 184.
Location/Qualifiers
1. 184
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/db_xref="taxon:4577"
/clone="ig24e03"
/lab_host="DH5a"
/clone_lib="WGS-ZmaysF (DH5a methyl filtered)"
/note="Organ: immature ears; Site_1: Xba I; Site_2: Xba I;
The vector was digested with XbaI and one nucleotide was
added by fill in in the recessive 3' end. The genomic DNA
was nebulized, end repaired, adaptor ligated and size
fractionated using sephadex. The resulting fragments were
between 0.8 and 3 kb and were cloned into the vector (.x/y
reads in M13mp19, .b/g reads in pUC19). The same ligation
was transformed into DH5a."

ORIGIN

Query Match 18.1%; Score 27.8; DB 8; Length 184;
Best Local Similarity 62.0%; Pred. No. 5e+03;
Matches 44; Conservative 0; Mismatches 27; Indels 0; Gaps 0;
QY 67 CGAGTCGGCGCCCGCGACTCGACGATGAGCGAGATGACCGCGCCGCGACTCGA 126
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 112 CGACGCGCGCGTCGCGGACGTGAAGGACAGACTGACAGCGCTGCTCCGCTCCGCTCGC 171
QY 127 CGATGAGCGAG 137
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 172 CGACAAAGCGCG 182

Search completed: April 9, 2005, 02:31:57
Job time : 3011 secs



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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 9, 2005, 01:03:52 ; Search time 494 Seconds
(without alignments)
1889.151 Million cell updates/sec

Title: US-09-887-194A-13

Perfect score: 154
Sequence: 1 cggcgcgagctggtcatctc.....gagatgaccagctccgcg 154

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5615251 seqs, 3030001701 residues

Total number of hits satisfying chosen parameters: 5800676

Minimum DB seq length: 0
Maximum DB seq length: 200

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Published Applications NA:*

1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
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12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	154	100.0	154	10	US-09-887-194A-13 Sequence 13, Appl
3	154	100.0	154	10	US-09-934-900-25 Sequence 25, Appl
4	154	100.0	154	10	US-09-934-900-25 Sequence 25, Appl
5	154	100.0	154	18	US-10-734-947-7 Sequence 7, Appl1
6	154	100.0	154	18	US-10-734-947-7 Sequence 7, Appl1
7	154	100.0	154	19	US-10-981-293-25 Sequence 25, Appl
8	154	100.0	154	19	US-10-981-293-25 Sequence 25, Appl
9	80	51.9	80	10	US-09-887-194A-12 Sequence 12, Appl
10	80	51.9	80	10	US-09-887-194A-12 Sequence 12, Appl
11	80	51.9	80	10	US-09-934-900-24 Sequence 24, Appl

C	12	80	51.9	80	10	US-09-934-900-24	Sequence 24, Appl
C	13	80	51.9	80	19	US-10-981-293-24	Sequence 24, Appl
C	14	80	51.9	80	19	US-10-981-293-24	Sequence 24, Appl
C	15	80	51.9	92	10	US-09-887-194A-14	Sequence 14, Appl
C	16	80	51.9	92	10	US-09-887-194A-14	Sequence 14, Appl
C	17	28.4	18.4	191	18	US-10-425-115-158821	Sequence 158821,
C	18	28.4	18.4	191	18	US-10-425-115-158821	Sequence 9894, Ap
C	19	27.4	17.8	175	18	US-10-437-963-9894	Sequence 9894, Ap
C	20	27.4	17.8	175	18	US-10-437-963-9894	Sequence 31230, A
C	21	26	16.9	195	18	US-10-437-963-31230	Sequence 31230, A
C	22	26	16.9	195	18	US-10-437-963-31230	Sequence 34, Appl
C	23	25	16.2	123	10	US-09-876-235-34	Sequence 34, Appl
C	24	25	16.2	123	10	US-09-876-235-34	Sequence 34, Appl
C	25	25	16.2	123	18	US-10-764-799-34	Sequence 34, Appl
C	26	25	16.2	123	18	US-10-764-799-34	Sequence 21853, A
C	27	24.8	16.1	108	16	US-10-029-386-21853	Sequence 21853, A
C	28	24.8	16.1	108	16	US-10-029-386-21853	Sequence 21754, A
C	29	24.6	16.0	167	18	US-10-767-701-21754	Sequence 21754, A
C	30	24.6	16.0	167	18	US-10-767-701-21754	Sequence 4668, Ap
C	31	24.4	15.8	164	9	US-09-923-876-4668	Sequence 4668, Ap
C	32	24.4	15.8	164	9	US-09-923-876-4668	Sequence 4668, Ap
C	33	24.4	15.8	164	10	US-09-923-876-4668	Sequence 4668, Ap
C	34	24.4	15.8	164	10	US-09-923-876-4668	Sequence 4668, Ap
C	35	24.4	15.8	183	18	US-10-425-115-62701	Sequence 62701, A
C	36	24.4	15.8	183	18	US-10-425-115-62701	Sequence 62701, A
C	37	24.4	15.8	185	9	US-09-864-761-25686	Sequence 25686, A
C	38	24.4	15.8	185	9	US-09-864-761-25686	Sequence 25686, A
C	39	24.2	15.7	175	18	US-10-753-646-15	Sequence 15, Appl
C	40	24.2	15.7	175	18	US-10-753-646-15	Sequence 15, Appl
C	41	24.2	15.7	183	18	US-10-425-115-140476	Sequence 140476,
C	42	24.2	15.7	183	18	US-10-425-115-140476	Sequence 140476,
C	43	23.6	15.3	192	15	US-10-156-761-3130	Sequence 3130, Ap
C	44	23.6	15.3	192	15	US-10-156-761-3130	Sequence 3130, Ap
C	45	23.4	15.2	155	18	US-10-425-115-22757	Sequence 22757, A
C	46	23.4	15.2	155	18	US-10-425-115-22757	Sequence 22757, A
C	47	23.4	15.2	159	18	US-10-437-963-58822	Sequence 58822, A
C	48	23.4	15.2	159	18	US-10-437-963-58822	Sequence 58822, A
C	49	23.4	15.2	192	15	US-10-156-761-6669	Sequence 6669, Ap
C	50	23.4	15.2	192	15	US-10-156-761-6669	Sequence 6669, Ap
C	51	23.2	15.1	151	18	US-10-425-115-127884	Sequence 127884,
C	52	23.2	15.1	151	18	US-10-425-115-127884	Sequence 127884,
C	53	23.2	15.1	166	18	US-10-767-701-18290	Sequence 18290, A
C	54	23.2	15.1	166	18	US-10-767-701-18290	Sequence 18290, A
C	55	23.2	15.1	192	9	US-09-920-300A-496	Sequence 496, App
C	56	23.2	15.1	192	9	US-09-920-300A-496	Sequence 496, App
C	57	23.2	15.1	192	13	US-10-033-528-496	Sequence 496, App
C	58	23.2	15.1	192	13	US-10-033-528-496	Sequence 496, App
C	59	23.2	15.1	192	16	US-10-099-926-496	Sequence 28, Appl
C	60	23.2	15.1	192	16	US-10-099-926-496	Sequence 28, Appl
C	61	23	14.9	74	17	US-10-434-156-28	Sequence 28, Appl
C	62	23	14.9	74	17	US-10-434-156-28	Sequence 28, Appl
C	63	23	14.9	176	10	US-09-862-540-7	Sequence 7, Appli
C	64	23	14.9	176	10	US-09-862-540-7	Sequence 7, Appli
C	65	23	14.9	192	18	US-10-425-115-81742	Sequence 81742, A
C	66	23	14.9	192	18	US-10-425-115-81742	Sequence 81742, A
C	67	23	14.9	192	18	US-10-425-115-95527	Sequence 95527, A
C	68	23	14.9	192	18	US-10-425-115-95527	Sequence 95527, A
C	69	22.8	14.8	137	18	US-10-425-115-2476	Sequence 2476, Ap
C	70	22.8	14.8	137	18	US-10-425-115-2476	Sequence 2476, Ap
C	71	22.8	14.8	171	18	US-10-425-115-74791	Sequence 74791, A
C	72	22.8	14.8	171	18	US-10-425-115-74791	Sequence 74791, A
C	73	22.8	14.8	195	18	US-10-425-115-162391	Sequence 162391,
C	74	22.8	14.8	195	18	US-10-425-115-162391	Sequence 162391,
C	75	22.8	14.8	199	18	US-10-425-115-97978	Sequence 97978, A
C	76	22.8	14.8	199	18	US-10-425-115-97978	Sequence 97978, A
C	77	22.6	14.7	180	15	US-10-156-761-4433	Sequence 4433, Ap
C	78	22.6	14.7	180	15	US-10-156-761-4433	Sequence 4433, Ap
C	79	22.6	14.7	183	17	US-10-140-410-1	Sequence 1, Appli
C	80	22.6	14.7	183	17	US-10-140-410-1	Sequence 1, Appli
C	81	22.6	14.7	200	11	US-09-987-899-107	Sequence 107, App
C	82	22.6	14.7	200	11	US-09-987-899-107	Sequence 107, App
C	83	22.4	14.5	110	19	US-10-950-009-970	Sequence 970, App
C	84	22.4	14.5	110	19	US-10-950-009-970	Sequence 970, App

85	22.4	14.5	114	18	US-10-741-601-2931	Sequence 2931, Ap
C	86	22.4	14.5	114	18	US-10-741-601-2931
	87	22.4	14.5	114	18	US-10-741-601-3022
C	88	22.4	14.5	114	18	US-10-741-601-3022
	89	22.4	14.5	114	18	US-10-741-601-3115
C	90	22.4	14.5	114	18	US-10-741-601-3115
	91	22.4	14.5	114	19	US-10-741-600-11671
C	92	22.4	14.5	114	19	US-10-741-600-11671
	93	22.4	14.5	114	19	US-10-741-600-11762
C	94	22.4	14.5	114	19	US-10-741-600-11762
	95	22.4	14.5	114	19	US-10-741-600-11855
C	96	22.4	14.5	114	19	US-10-741-600-11855
	97	22.4	14.5	151	18	US-10-425-115-3104
C	98	22.4	14.5	151	18	US-10-425-115-3104
	99	22.4	14.5	161	17	US-10-424-599-56083
C	100	22.4	14.5	161	17	US-10-424-599-56083

ALIGNMENTS

```
RESULT 1
US-09-887-194A-13
; Sequence 13, Application US/09887194A
; Publication No. US20030036197A1
; GENERAL INFORMATION:
; APPLICANT: Glassman, Kimberly F.
; APPLICANT: Gordon-Kamm, William J.
; APPLICANT: Kinney, Anthony
; APPLICANT: Lowe, Keith S.
; APPLICANT: Nichols, Scott E.
; APPLICANT: Stecca, Kevin L.
; TITLE OF INVENTION: RECOMBINANT CONSTRUCTS AND THEIR USE IN REDUCING GENE EXPRESSION
; FILE REFERENCE: BBI449 US NA
; CURRENT APPLICATION NUMBER: US/09/887,194A
; CURRENT FILING DATE: 2002-03-13
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 13
; LENGTH: 154
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: ELVISLIVES complementary
; OTHER INFORMATION: region of PKS133
US-09-887-194A-13
```

```
Query Match          100.0%; Score 154; DB 10; Length 154;
Best Local Similarity 100.0%; Pred. No. 2.2e-37;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGCGGAGCTGTCATCTCGCTCATCTCGAGTCGGCGCGGAGCTGTCATCTCGCT 60
    |||
Db 1 CGGCGGAGCTGTCATCTCGCTCATCTCGAGTCGGCGCGGAGCTGTCATCTCGCT 60

QY 61 CATCGTCAGTCGGCGCGCGCGGAGTCGACGATGAGCGAGATGACCACTCCGGCGCGG 120
    |||
Db 61 CATCGTCAGTCGGCGCGCGCGGAGTCGACGATGAGCGAGATGACCACTCCGGCGCGG 120

QY 121 ACTCGACGATGAGCGGAGATGACCACTCCGGCGCGG 154
    |||
Db 121 ACTCGACGATGAGCGGAGATGACCACTCCGGCGCGG 154
```

```
RESULT 2
US-09-887-194A-13/c
; Sequence 13, Application US/09887194A
; Publication No. US20030036197A1
; GENERAL INFORMATION:
; APPLICANT: Glassman, Kimberly F.
; APPLICANT: Gordon-Kamm, William J.
; APPLICANT: Kinney, Anthony
; APPLICANT: Lowe, Keith S.
```

```
; APPLICANT: Nichols, Scott E.
; APPLICANT: Stecca, Kevin L.
; TITLE OF INVENTION: RECOMBINANT CONSTRUCTS AND THEIR USE IN REDUCING GENE EXPRESSION
; FILE REFERENCE: BBI449 US NA
; CURRENT APPLICATION NUMBER: US/09/887,194A
; CURRENT FILING DATE: 2002-03-13
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 13
; LENGTH: 154
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: ELVISLIVES complementary
; OTHER INFORMATION: region of PKS133
US-09-887-194A-13
```

```
Query Match          100.0%; Score 154; DB 10; Length 154;
Best Local Similarity 100.0%; Pred. No. 2.2e-37;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGCGGAGCTGTCATCTCGCTCATCTCGAGTCGGCGCGGAGCTGTCATCTCGCT 60
    |||
Db 154 CGGCGGAGCTGTCATCTCGCTCATCTCGAGTCGGCGCGGAGCTGTCATCTCGCT 95

QY 61 CATCGTCAGTCGGCGCGCGCGGAGTCGACGATGAGCGAGATGACCACTCCGGCGCGG 120
    |||
Db 94 CATCGTCAGTCGGCGCGCGCGGAGTCGACGATGAGCGAGATGACCACTCCGGCGCGG 35

QY 121 ACTCGACGATGAGCGGAGATGACCACTCCGGCGCGG 154
    |||
Db 34 ACTCGACGATGAGCGGAGATGACCACTCCGGCGCGG 1
```

```
RESULT 3
US-09-934-900-25
; Sequence 25, Application US/09934900
; Publication No. US20030054521A1
; GENERAL INFORMATION:
; APPLICANT: Booth, Russ
; APPLICANT: Cahoon, Rebecca E
; APPLICANT: Hitz, William D
; APPLICANT: Kinney, Anthony
; APPLICANT: Yaday, Naren
; TITLE OF INVENTION: Nucleotide Sequences of a New Class of Diverged Delta-9 Stearoyl-
; TITLE OF INVENTION: ACP Desaturase
; FILE REFERENCE: BBI476 US NA
; CURRENT APPLICATION NUMBER: US/09/934,900
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/226996
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 25
; LENGTH: 154
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: ELVISLIVES complementary
; OTHER INFORMATION: region of PKS133
US-09-934-900-25
```

```
Query Match          100.0%; Score 154; DB 10; Length 154;
Best Local Similarity 100.0%; Pred. No. 2.2e-37;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGCGGAGCTGTCATCTCGCTCATCTCGAGTCGGCGCGGAGCTGTCATCTCGCT 60
    |||
Db 1 CGGCGGAGCTGTCATCTCGCTCATCTCGAGTCGGCGCGGAGCTGTCATCTCGCT 60

QY 61 CATCGTCAGTCGGCGCGCGCGGAGTCGACGATGAGCGAGATGACCACTCCGGCGCGG 120
    |||
Db 61 CATCGTCAGTCGGCGCGCGCGGAGTCGACGATGAGCGAGATGACCACTCCGGCGCGG 120
```



```

; TITLE OF INVENTION: ACP Desaturase
; FILE REFERENCE: BB1476 US NA
; CURRENT APPLICATION NUMBER: US/10/981,293
; CURRENT FILING DATE: 2004-11-04
; PRIOR APPLICATION NUMBER: US/09/934,900
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/226996
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 25
; LENGTH: 154
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: ELVISLIVES complementary
; OTHER INFORMATION: region of pKS133
US-10-981-293-25
```

```

Query Match      100.0%; Score 154; DB 19; Length 154;
Best Local Similarity 100.0%; Pred. No. 2.2e-37;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY      1 CGGCCGAGCTGTCATCTCGCTCATCTCGAGTCGGCGCCGAGCTGTGTCATCTCGCT 60
        |||
        1 CGGCCGAGCTGTCATCTCGCTCATCTCGAGTCGGCGCCGAGCTGTGTCATCTCGCT 60
Db
QY      61 CATCGTCGAGTCGGCGCCGCGGCTCGACGATGAGCGAGATGACCACTCCGGCCGCG 120
        |||
        61 CATCGTCGAGTCGGCGCCGCGGCTCGACGATGAGCGAGATGACCACTCCGGCCGCG 120
Db
QY      121 ACTCGACGATGAGCGAGATGACCACTCCGGCCG 154
        |||
        121 ACTCGACGATGAGCGAGATGACCACTCCGGCCG 154
Db
```

RESULT 8

```

US-10-981-293-25/c
; Sequence 25, Application US/10981293
; Publication No. US20050066390A1
; GENERAL INFORMATION:
; APPLICANT: Booth, Russ
; APPLICANT: Cahoon, Rebecca E
; APPLICANT: Hiltz, William D
; APPLICANT: Kinney, Anthony
; APPLICANT: Yadav, Naren
; TITLE OF INVENTION: Nucleotide Sequences of a New Class of Diverged Delta-9 Stearoyl-
; TITLE OF INVENTION: ACP Desaturase
; FILE REFERENCE: BB1476 US NA
; CURRENT APPLICATION NUMBER: US/10/981,293
; CURRENT FILING DATE: 2004-11-04
; PRIOR APPLICATION NUMBER: US/09/934,900
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/226996
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 25
; LENGTH: 154
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: ELVISLIVES complementary
; OTHER INFORMATION: region of pKS133
US-10-981-293-25
```

```

Query Match      100.0%; Score 154; DB 19; Length 154;
Best Local Similarity 100.0%; Pred. No. 2.2e-37;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY      1 CGGCCGAGCTGTCATCTCGCTCATCTCGAGTCGGCGCCGAGCTGTGTCATCTCGCT 60
        |||
        154 CGGCCGAGCTGTCATCTCGCTCATCTCGAGTCGGCGCCGAGCTGTGTCATCTCGCT 95
Db
```

```

QY      61 CATCGTCGAGTCGGCGCCGCGGCTCGACGATGAGCGAGATGACCACTCCGGCCGCG 120
        |||
        94 CATCGTCGAGTCGGCGCCGCGGCTCGACGATGAGCGAGATGACCACTCCGGCCGCG 35
Db
QY      121 ACTCGACGATGAGCGAGATGACCACTCCGGCCG 154
        |||
        34 ACTCGACGATGAGCGAGATGACCACTCCGGCCG 1
Db
```

RESULT 9

```

US-09-887-194A-12
; Sequence 12, Application US/09887194A
; Publication No. US20030036197A1
; GENERAL INFORMATION:
; APPLICANT: Glasman, Kimberly F.
; APPLICANT: Gordon-Kamm, William J.
; APPLICANT: Kinney, Anthony
; APPLICANT: Lowe, Keith S.
; APPLICANT: Nichols, Scott E.
; APPLICANT: Stecca, Kevin L.
; TITLE OF INVENTION: RECOMBINANT CONSTRUCTS AND THEIR USE IN REDUCING GENE EXPRESSION
; FILE REFERENCE: BB1449 US NA
; CURRENT APPLICATION NUMBER: US/09/887,194A
; CURRENT FILING DATE: 2002-03-13
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 12
; LENGTH: 80
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: ELVISLIVES complementary
; OTHER INFORMATION: region of pKS106 and pKS124
US-09-887-194A-12
```

```

Query Match      51.9%; Score 80; DB 10; Length 80;
Best Local Similarity 100.0%; Pred. No. 6.3e-15;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY      38 CGGCCGAGCTGTCATCTCGCTCATCTCGAGTCGGCGCCGCGGCTCGACGATGAGC 97
        |||
        1 CGGCCGAGCTGTCATCTCGCTCATCTCGAGTCGGCGCCGCGGCTCGACGATGAGC 60
Db
QY      98 GAGATGACCACTCCGGCCG 117
        |||
        61 GAGATGACCACTCCGGCCG 80
Db
```

RESULT 10

```

US-09-887-194A-12/c
; Sequence 12, Application US/09887194A
; Publication No. US20030036197A1
; GENERAL INFORMATION:
; APPLICANT: Glasman, Kimberly F.
; APPLICANT: Gordon-Kamm, William J.
; APPLICANT: Kinney, Anthony
; APPLICANT: Lowe, Keith S.
; APPLICANT: Nichols, Scott E.
; APPLICANT: Stecca, Kevin L.
; TITLE OF INVENTION: RECOMBINANT CONSTRUCTS AND THEIR USE IN REDUCING GENE EXPRESSION
; FILE REFERENCE: BB1449 US NA
; CURRENT APPLICATION NUMBER: US/09/887,194A
; CURRENT FILING DATE: 2002-03-13
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 12
; LENGTH: 80
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: ELVISLIVES complementary
; OTHER INFORMATION: region of pKS106 and pKS124
```



```
; APPLICANT: Cahoon, Rebecca E
; APPLICANT: Hiltz, William D
; APPLICANT: Kinney, Anthony
; APPLICANT: Yadav, Naren
; TITLE OF INVENTION: Nucleotide Sequences of a New Class of Diverged Delta-9 Stearoyl-
; FILE REFERENCE: BBI476 US NA
; CURRENT APPLICATION NUMBER: US/10/981,293
; CURRENT FILING DATE: 2004-11-04
; PRIOR APPLICATION NUMBER: US/09/934,900
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/226996
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 24
; LENGTH: 80
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: ELVISLIVES complementary
US-10-981-293-24
```

```
Query Match          51.9%; Score 80; DB 19; Length 80;
Best Local Similarity 100.0%; Pred. No. 6.3e-15;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 38 CGGCCGAGCTGTCATCTCGCTCATCTCGAGTCGCGCGCGCCGACTCGACGATGAGC 97
    |||
Db 80 CGGCCGAGCTGTCATCTCGCTCATCTCGAGTCGCGCGCGCCGACTCGACGATGAGC 21
    |||

QY 98 GAGATGACCACTCCGCCG 117
    |||
Db 20 GAGATGACCACTCCGCCG 1
    |||
```

RESULT 15

```
US-09-887-194A-14
; Sequence 14, Application US/09887194A
; Publication No. US20030036197A1
; GENERAL INFORMATION:
; APPLICANT: Glassman, Kimberly F.
; APPLICANT: Gordon-Kamm, William J.
; APPLICANT: Kinney, Anthony
; APPLICANT: Lowe, Keith S.
; APPLICANT: Nichols, Scott E.
; APPLICANT: Stecca, Kevin L.
; TITLE OF INVENTION: RECOMBINANT CONSTRUCTS AND THEIR USE IN REDUCING GENE EXPRESSION
; FILE REFERENCE: BBI449 US NA
; CURRENT APPLICATION NUMBER: US/09/887,194A
; CURRENT FILING DATE: 2002-03-13
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 14
; LENGTH: 92
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: ELVISLIVES PCR primer
US-09-887-194A-14
```

```
Query Match          51.9%; Score 80; DB 10; Length 92;
Best Local Similarity 100.0%; Pred. No. 6.2e-15;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 38 CGGCCGAGCTGTCATCTCGCTCATCTCGAGTCGCGCGCGCCGACTCGACGATGAGC 97
    |||
Db 7 CGGCCGAGCTGTCATCTCGCTCATCTCGAGTCGCGCGCGCCGACTCGACGATGAGC 66
    |||

QY 98 GAGATGACCACTCCGCCG 117
    |||
Db 67 GAGATGACCACTCCGCCG 86
    |||
```

```
RESULT 16
US-09-887-194A-14/c
; Sequence 14, Application US/09887194A
; Publication No. US20030036197A1
; GENERAL INFORMATION:
; APPLICANT: Glassman, Kimberly F.
; APPLICANT: Gordon-Kamm, William J.
; APPLICANT: Kinney, Anthony
; APPLICANT: Lowe, Keith S.
; APPLICANT: Nichols, Scott E.
; APPLICANT: Stecca, Kevin L.
; TITLE OF INVENTION: RECOMBINANT CONSTRUCTS AND THEIR USE IN REDUCING GENE EXPRESSION
; FILE REFERENCE: BBI449 US NA
; CURRENT APPLICATION NUMBER: US/09/887,194A
; CURRENT FILING DATE: 2002-03-13
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 14
; LENGTH: 92
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: ELVISLIVES PCR primer
US-09-887-194A-14
```

```
Query Match          51.9%; Score 80; DB 10; Length 92;
Best Local Similarity 100.0%; Pred. No. 6.2e-15;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 38 CGGCCGAGCTGTCATCTCGCTCATCTCGAGTCGCGCGCGCCGACTCGACGATGAGC 97
    |||
Db 86 CGGCCGAGCTGTCATCTCGCTCATCTCGAGTCGCGCGCGCCGACTCGACGATGAGC 27
    |||

QY 98 GAGATGACCACTCCGCCG 117
    |||
Db 26 GAGATGACCACTCCGCCG 7
    |||
```

RESULT 17

```
US-10-425-115-158821
; Sequence 158821, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 158821
; LENGTH: 191
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_76420C.1
US-10-425-115-158821
```

```
Query Match          18.4%; Score 28.4; DB 18; Length 191;
Best Local Similarity 52.5%; Pred. No. 27;
Matches 62; Conservative 0; Mismatches 56; Indels 0; Gaps 0;
```

```
QY 21 GCTCATCTGTCAGTCGCGCGCGAGCTGTCATCTCGCTCATCTGAGTCGCGCGCGC 80
    |||
Db 17 GCTCCGCTTGACCGGGGGACATCGGGGCGCATCGAGCTTACGAGCTGTTCATGAACG 76
    |||

QY 81 CGACTCGACGATGAGGAGATGACCACTCCGCCCGCCGACTCGACGATGAGGAGA 138
    |||
```

Db 77 CCATCACGGTGTGTAGAGATGTGGATGCCCTCCGCTTACAGACGACGACGCGCA 134

RESULT 18

US-10-425-115-158821/C

; Sequence 158821, Application US/10425115
; Publication No. US20040214272A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.

; APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

; TITLE OF INVENTION: Plants

; FILE REFERENCE: 38-21(53222)B

; CURRENT APPLICATION NUMBER: US/10/425,115

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 369326

; SEQ ID NO 158821

; LENGTH: 191

; TYPE: DNA

; ORGANISM: Zea mays

; FEATURE:

; OTHER INFORMATION: Clone ID: MRT4577_76420C.1

US-10-425-115-158821

Query Match 18.4%; Score 28.4; DB 18; Length 191;

Best Local Similarity 52.5%; Pred. No. 27;

Matches 62; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

Qy 17 TCTCGCTCATCTGAGTCGGCGCGGAGCTGTCTATCTGCTCATCTCGAGTCGCG 76

Db 134 TCGCCGTCGTCCTCTCTAGGCGGAGCATTCAGCATCTTACAGACCGTGATGCG 75

Qy 77 GCCGCCGACTCGAGATGAGCGAGATGACCACTCCGCCGCACTCGACGATGAGC 134

Db 74 TTATGAACAGCTCGTAGGCTGCGATGGCGCCGATGTCCCGGTCAAGCGGAGC 17

RESULT 19

US-10-437-963-9894

; Sequence 9894, Application US/10437963

; Publication No. US20040123343A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.

; APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei

; APPLICANT: Wu, Wei

; APPLICANT: Boukharov, Andrey A.

; APPLICANT: Barbazuk, Brad

; APPLICANT: Li, Ping

; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

; FILE REFERENCE: 38-21(53221)B

; CURRENT APPLICATION NUMBER: US/10/437,963

; CURRENT FILING DATE: 2003-05-14

; NUMBER OF SEQ ID NOS: 204966

; SEQ ID NO 9894

; LENGTH: 175

; TYPE: DNA

; ORGANISM: Oryza sativa

; FEATURE:

; OTHER INFORMATION: Clone ID: PAT_MRT4530_16268C.1

US-10-437-963-9894

Query Match 17.8%; Score 27.4; DB 18; Length 175;

Best Local Similarity 62.3%; Pred. No. 54;

Matches 43; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

Qy 64 CGTCGAGTCGGCGCGCGGAGCTGACGATGAGCGAGATGACGAGCTCCGCCGCGACT 123

Db 1 CGCCTAGCTACCGCGCCACCGCGGAGGAGCGGATGTCTCTGGGAGCATACA 60

Qy 124 CGACGATGA 132

Db 61 CACCCATGA 69

RESULT 20

US-10-437-963-9894/C

; Sequence 9894, Application US/10437963

; Publication No. US20040123343A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.

; APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei

; APPLICANT: Wu, Wei

; APPLICANT: Boukharov, Andrey A.

; APPLICANT: Barbazuk, Brad

; APPLICANT: Li, Ping

; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

; FILE REFERENCE: 38-21(53221)B

; CURRENT APPLICATION NUMBER: US/10/437,963

; CURRENT FILING DATE: 2003-05-14

; NUMBER OF SEQ ID NOS: 204966

; SEQ ID NO 9894

; LENGTH: 175

; TYPE: DNA

; ORGANISM: Oryza sativa

; FEATURE:

; OTHER INFORMATION: Clone ID: PAT_MRT4530_16268C.1

US-10-437-963-9894

Query Match 17.8%; Score 27.4; DB 18; Length 175;

Best Local Similarity 62.3%; Pred. No. 54;

Matches 43; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

Qy 23 TCATGTCGAGTCGGCGCGGAGCTGTCTATCTGCTCATCTCGAGTCGCGCGGCC 82

Db 69 TCATGGGTGTGTATCTGTCGCCGAGCAGACATTCGGCTCTCTCGCGGTCGCGGCGTA 10

Qy 83 GACTCGAGC 91

Db 9 GCCTAGGCG 1

RESULT 21

US-10-437-963-31230

; Sequence 31230, Application US/10437963

; Publication No. US20040123343A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.

; APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei

; APPLICANT: Wu, Wei

; APPLICANT: Boukharov, Andrey A.

; APPLICANT: Barbazuk, Brad

; APPLICANT: Li, Ping

; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

; FILE REFERENCE: 38-21(53221)B

; CURRENT APPLICATION NUMBER: US/10/437,963

; CURRENT FILING DATE: 2003-05-14

; NUMBER OF SEQ ID NOS: 204966

; SEQ ID NO 31230

; LENGTH: 195

; TYPE: DNA

; ORGANISM: Oryza sativa

; FEATURE:

; OTHER INFORMATION: Clone ID: PAT_MRT4530_35558C.1

US-10-437-963-31230


```
Query Match: 16.9%; Score 26; DB 18; Length 195;
Best Local Similarity 54.1%; Pred. No. 1.4e+02;
Matches 53; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

OY 51 TCATCTGCTCATGCTGAGTGGCGCCCGACTCGACGATGAGGATGACGACT 110
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 41 TCGCCGCTCCCTGCTGCTGCGCTGACGGCGACCGACCGCGCGCGCTCT 100
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

OY 111 CCGCGCCGCGACTGACGATGAGCGAGATGACGACTC 148
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 101 CCGACGCGCGCCCGCGCTTTAAGACATGAGTATCGC 138

RESULT 22
US-10-437-963-31230/c
; Sequence 31230, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 31230
; LENGTH: 195
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_35558C.1
US-10-437-963-31230

Query Match: 16.9%; Score 26; DB 18; Length 195;
Best Local Similarity 54.1%; Pred. No. 1.4e+02;
Matches 53; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

OY 7 GAGCTGCTATCTGCTCATGCTGAGTGGCGCCGCGACTGTCATCTCGCTCATCGT 66
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 138 GCGATACTATGTTCTTTAAACGCGGGGCGCGCTCGAGACGGCGCGCGTCCGCGCGC 79
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

OY 67 CGAGTCGGCGCCCGCGACTCGACGATGAGCGAGATGA 104
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 78 GTGTCGGCTGCGCTGACGCGACGAGGAGCGCGCGCA 41

RESULT 23
US-09-876-235-34
; Sequence 34, Application US/09876235
; Publication No. US20030022236A1
; GENERAL INFORMATION:
; APPLICANT: Szostak, Jack W.
; APPLICANT: Roberts, Richard W.
; APPLICANT: Liu, Rihe
; TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
; TITLE OF INVENTION: FUSIONS
; FILE REFERENCE: 00786/350005
; CURRENT APPLICATION NUMBER: US/09/876,235
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/247,190
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/035,963
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-01-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/064,491
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-11-06
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/007,005
```

```
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-01-14
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 123
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: n = a, g, t, or c. s = c or g.
US-09-876-235-34

Query Match: 16.2%; Score 25; DB 10; Length 123;
Best Local Similarity 15.0%; Pred. No. 2.9e+02;
Matches 16; Conservative 26; Mismatches 65; Indels 0; Gaps 0;

OY 18 CTGCTCATGCTGAGTGGCGCCCGAGCTGTGTCATCTGCTCATGCTGAGTGGCGG 77
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 12 CTGTGTCATCSNNSNNSNNSNNSNNSNNSNNSNNSNNSNNSNNSNNSN 71
    : : : : : : : : : : : : : : : : : : : : : : : :

OY 78 CCGCCGACTCGACGATGAGCGAGATGACGACTCCGCGCGCGACTC 124
    : : : : : : : : : : : : : : : : : : : : : : : :
DB 72 NSNNSNNSNNSNNSNNSNNSNNSNNSNNSNNSNNSNNSNCTCTCGCCCTTGCTC 118
    : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 24
US-09-876-235-34/c
; Sequence 34, Application US/09876235
; Publication No. US20030022236A1
; GENERAL INFORMATION:
; APPLICANT: Szostak, Jack W.
; APPLICANT: Roberts, Richard W.
; APPLICANT: Liu, Rihe
; TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
; TITLE OF INVENTION: FUSIONS
; FILE REFERENCE: 00786/350005
; CURRENT APPLICATION NUMBER: US/09/876,235
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/247,190
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/035,963
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-01-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/064,491
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-11-06
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/007,005
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 123
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: n = a, g, t, or c. s = c or g.
US-09-876-235-34

Query Match: 16.2%; Score 25; DB 10; Length 123;
Best Local Similarity 15.0%; Pred. No. 2.9e+02;
Matches 16; Conservative 26; Mismatches 65; Indels 0; Gaps 0;

OY 31 GAGTCGGCGCCCGAGCTGTGTCATCTGCTCATGCTGAGTGGCGCCCGCGACTCGAC 90
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 118 GAGCAAGGGCGAGAGNNSNNSNNSNNSNNSNNSNNSNNSNNSNNSNNSN 59
    : : : : : : : : : : : : : : : : : : : : : : : :

OY 91 GATGAGCGAGATGACGACTCCGCGCGCGCGACTCGACGATGAGCGAG 137
    : : : : : : : : : : : : : : : : : : : : : : : :
DB 58 SNNSNNSNNSNNSNNSNNSNNSNNSNNSNNSNNSNNSNNSGATGCAAG 12
    : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 25
US-10-764-799-34
; Sequence 34, Application US/10764799
; Publication No. US20040253612A1
; GENERAL INFORMATION:
```

```

; APPLICANT: Szostak, Jack W.
; APPLICANT: Roberts, Richard W.
; TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
; TITLE OF INVENTION: FUSIONS
; FILE REFERENCE: 00786/350005
; CURRENT APPLICATION NUMBER: US/10/764,799
; PRIOR FILING DATE: 2004-01-26
; PRIOR APPLICATION NUMBER: US/09/247,190
; PRIOR FILING DATE: 1999-02-09
; PRIOR APPLICATION NUMBER: 60/035,963
; PRIOR FILING DATE: 1997-01-21
; PRIOR APPLICATION NUMBER: 60/064,491
; PRIOR FILING DATE: 1997-11-06
; PRIOR APPLICATION NUMBER: 09/007,005
; PRIOR FILING DATE: 1998-01-14
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 123
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: n = a, g, t, or c. s = c or g.
US-10-764-799-34

```

```

Query Match      16.2%; Score 25; DB 18; Length 123;
Best Local Similarity 15.0%; Pred. No. 2.9e+02;
Matches 16; Conservative 26; Mismatches 65; Indels 0; Gaps 0;

```

```

Qy      18 CTGCTCATGTCGAGTCGGCGCGGAGCTGTCATCTGCTCATGTCGAGTCGGCGG 77
      ||| ||| ||| : : : : : : : : : : : : : : : : : :
Db      12 CTGTGTCATCSNNSNNSNNSNNSNNSNNSNNSNNSNNSNNSNNSNNSN 71
Qy      78 CCGCCGACTGACGATGAGCGAGATGACCACTCCGCGCCGCACTC 124
      : : : : : : : : : : : : : : : : : :
Db      72 NSNNSNNSNNSNNSNNSNNSNNSNNSNNSNNSNNSNNSNCTCCTCGCCCTTGCTC 118

```

RESULT 26

```

US-10-764-799-34/c
; Sequence 34, Application US/10764799
; Publication No. US20040253612A1
; GENERAL INFORMATION:
; APPLICANT: Szostak, Jack W.
; APPLICANT: Roberts, Richard W.
; APPLICANT: Liu, Rihe
; TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
; TITLE OF INVENTION: FUSIONS
; FILE REFERENCE: 00786/350005
; CURRENT APPLICATION NUMBER: US/10/764,799
; CURRENT FILING DATE: 2004-01-26
; PRIOR APPLICATION NUMBER: US/09/247,190
; PRIOR FILING DATE: 1999-02-09
; PRIOR APPLICATION NUMBER: 60/035,963
; PRIOR FILING DATE: 1997-01-21
; PRIOR APPLICATION NUMBER: 60/064,491
; PRIOR FILING DATE: 1997-11-06
; PRIOR APPLICATION NUMBER: 09/007,005
; PRIOR FILING DATE: 1998-01-14
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 123
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: n = a, g, t, or c. s = c or g.
US-10-764-799-34

```

```

Query Match      16.2%; Score 25; DB 18; Length 123;
Best Local Similarity 15.0%; Pred. No. 2.9e+02;
Matches 16; Conservative 26; Mismatches 65; Indels 0; Gaps 0;

```

```

Qy      31 GAGTCGGCGCGCGGAGCTGTCTATCTCGCTCATGTCGAGTCGGCGCGCGCACTCGAC 90
      ||| ||| ||| : : : : : : : : : : : : : : : : : :
Db      118 GAGCAAGGGCGGAGGAGNNSNNSNNSNNSNNSNNSNNSNNSNNSN 59
Qy      91 GATGACGAGATGACCACTCCGCGCGCGCACTCGACGATGACGAG 137
      : : : : : : : : : : : : : : : : : :
Db      58 SNNSNNSNNSNNSNNSNNSNNSNNSNNSNNSNNSNNSNNGATGCACAAG 12

```

RESULT 27

```

US-10-029-386-21853
; Sequence 21853, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
; FILE REFERENCE: ABOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 21853
; LENGTH: 108
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO CHR19.3
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.4
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.2
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.7
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.5
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.8
; OTHER INFORMATION: NT HIT: AP166267.1, EVALUE 2.00e-08
; OTHER INFORMATION: SWISSPROT HIT: Q05090, EVALUE 3.00e-03
; OTHER INFORMATION: EST_HUMAN HIT: BG122566.1, EVALUE 4.00e-54
US-10-029-386-21853

```

```

Query Match      16.1%; Score 24.8; DB 16; Length 108;
Best Local Similarity 72.7%; Pred. No. 3.4e+02;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

```

```

Qy      106 CAGCTCCGCGCGCGGAGCTGTCGATGAGCGAGATGACCACTCC 149
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      5 CTGCTCTGCGCGCGGCGCTCGCTCGAGCGGAGACCACTTC 48

```

RESULT 28

```

US-10-029-386-21853/c
; Sequence 21853, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
; FILE REFERENCE: ABOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 21853
; LENGTH: 108
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO CHR19.3
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.4
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.2

```

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.7
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.5
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.8
OTHER INFORMATION: NT HIT: AF166267.1, EVALUE 2.00e-08
OTHER INFORMATION: SWISSPROT HIT: Q05090, EVALUE 3.00e-03
OTHER INFORMATION: EST_HUMAN HIT: BG122566.1, EVALUE 4.00e-54
US-10-029-386-21853

Query Match 16.1%; Score 24.8; DB 16; Length 108;
Best Local Similarity 72.7%; Pred. No. 3.4e+02;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 6 GGAGCTGTCATCTCGCTCATCGTCAGTCGGCGCCGAGACTG 49
DB 48 GAAGCTGTCCTCCCGCTCCGAGCGGCGCGCGCAGAGCAG 5

RESULT 29

US-10-767-701-21754
Sequence 21754, Application US/10767701
Publication No. US20040172684A1
GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53535)B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 21754
LENGTH: 167
TYPE: DNA
ORGANISM: Sorghum bicolor
FEATURE:
OTHER INFORMATION: Clone ID: 13318234
US-10-767-701-21754

Query Match 16.0%; Score 24.6; DB 18; Length 167;
Best Local Similarity 57.0%; Pred. No. 3.8e+02;
Matches 45; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 2 GGCCGAGCTGTCATCTCGCTCATCGTCAGTCGGCGCCGAGACTGTCATCTCGCTC 61
DB 70 GGCGGAGCTTCTTCGGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTGC 129

QY 62 ATGCTGAGTCGGCGCGCG 80
DB 130 ATGCTGAGCGCGCGCGCG 148

RESULT 30

US-10-767-701-21754/c
Sequence 21754, Application US/10767701
Publication No. US20040172684A1
GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53535)B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 21754
LENGTH: 167
TYPE: DNA
ORGANISM: Sorghum bicolor
FEATURE:
OTHER INFORMATION: Clone ID: 13318234
US-10-767-701-21754

Query Match 16.0%; Score 24.6; DB 18; Length 167;
Best Local Similarity 57.0%; Pred. No. 3.8e+02;
Matches 45; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 75 CGCCCGCCGACTCGACGATGAGCGAGATGACCACTCCGGCCGCGCGCGCGCGCGCGCG 134
DB 148 CGCGCGCGCCTCCACCATGACACCGCGCGCGATCCGCGCGCGCGCGCGCGCGCGCG 89

QY 135 GAGATGACCAGCTCCGCC 153
DB 88 CCGCCGAGAAGCTCCCGCC 70

RESULT 31

US-09-923-876-4668
Sequence 4668, Application US/09923876
Patent No. US20020013958A1
GENERAL INFORMATION:
APPLICANT: Lalgudi, Raghunath V.
APPLICANT: Kamigaki, Laura Y. (Ito)
APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING
FILE REFERENCE: PL-0012-1 CON
CURRENT APPLICATION NUMBER: US/09/923,876
CURRENT FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: 09/298,329
PRIOR FILING DATE: 1999-04-21
PRIOR APPLICATION NUMBER: 60/085,331
PRIOR FILING DATE: 1998-05-05
NUMBER OF SEQ ID NOS: 6332
SOFTWARE: PERL Program
SEQ ID NO 4668
LENGTH: 164
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. US20020013958A1 700455577H1
US-09-923-876-4668

Query Match 15.8%; Score 24.4; DB 9; Length 164;
Best Local Similarity 60.6%; Pred. No. 4.4e+02;
Matches 40; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 22 CTCATCGTCGAGTCGGCGCGCGAGCTGTCATCTCGCTCATCGTCGAGTCGGCGCGCG 81
DB 74 CTCGACGACGATGCGGAGCGGATCTGGGCACTCTGCTGCTCGCGCGCTTGCCATCTT 133

QY 82 CGACTC 87
DB 134 CTTCTC 139

RESULT 32

US-09-923-876-4668/c
Sequence 4668, Application US/09923876
Patent No. US20020013958A1
GENERAL INFORMATION:
APPLICANT: Lalgudi, Raghunath V.
APPLICANT: Kamigaki, Laura Y. (Ito)
APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING
FILE REFERENCE: PL-0012-1 CON
CURRENT APPLICATION NUMBER: US/09/923,876
CURRENT FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: 09/298,329
PRIOR FILING DATE: 1999-04-21
PRIOR APPLICATION NUMBER: 60/085,331
PRIOR FILING DATE: 1998-05-05

```
; NUMBER OF SEQ ID NOS: 6332
; SOFTWARE: PERL Program
; SEQ ID NO 4668
; LENGTH: 164
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20020013958A1 700455577H1
; LOCATION: 150
; OTHER INFORMATION: a, t, c, g, or other
US-09-923-876-4668
```

```
Query Match          15.8%; Score 24.4; DB 9; Length 164;
Best Local Similarity 60.6%; Pred. No. 4.4e+02;
Matches 40; Conservative 0; Mismatches 26; Indels 0; Gaps 0;
```

```
QY 68 GAGTCGGCGCGCCGCGACTCGACGATGAGCGAGATGACCACTCCGGCCGCGACTCGAC 127
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 139 GAGAGAGATGGCGAGGCGCGCGACAGAGATGCCCATCCGCTTCCGCATCGTC 80
QY 128 GATGAG 133
    ||| |||
Db 79 GTCGAG 74
```

```
RESULT 33
US-09-923-876-4668
; Sequence 4668, Application US/09923876
; Publication No. US20030237110A9
; GENERAL INFORMATION:
; APPLICANT: Lalgudi, Raghunath V.
; APPLICANT: Kamigaki, Laura Y. (Ito)
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING
; FILE REFERENCE: PL-0012-1 CON
; CURRENT APPLICATION NUMBER: US/09/923,876
; CURRENT FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: 09/298,329
; PRIOR FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: 60/085,331
; PRIOR FILING DATE: 1998-05-05
; NUMBER OF SEQ ID NOS: 6332
; SOFTWARE: PERL Program
; SEQ ID NO 4668
; LENGTH: 164
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030237110A9 700455577H1
; NAME/KEY: unsure
; LOCATION: 150
; OTHER INFORMATION: a, t, c, g, or other
US-09-923-876-4668
```

```
Query Match          15.8%; Score 24.4; DB 10; Length 164;
Best Local Similarity 60.6%; Pred. No. 4.4e+02;
Matches 40; Conservative 0; Mismatches 26; Indels 0; Gaps 0;
```

```
QY 22 CTCATCGTCGAGTCGGCGCGCGAGCTGTCATCTCGTCATCTCGAGTCGGCGCGCC 81
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 74 CTCGACGACGATGCGGAGCGGAGCTGGGCATCTGCTGCTGCGCGCCTTCGCATCTT 133
QY 82 CGACTC 87
    ||| |||
Db 134 CTTCTC 139
```

```
RESULT 34
US-09-923-876-4668/c
; Sequence 4668, Application US/09923876
```

```
; Publication No. US20030237110A9
; GENERAL INFORMATION:
; APPLICANT: Lalgudi, Raghunath V.
; APPLICANT: Kamigaki, Laura Y. (Ito)
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING
; FILE REFERENCE: PL-0012-1 CON
; CURRENT APPLICATION NUMBER: US/09/923,876
; CURRENT FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: 09/298,329
; PRIOR FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: 60/085,331
; PRIOR FILING DATE: 1998-05-05
; NUMBER OF SEQ ID NOS: 6332
; SOFTWARE: PERL Program
; SEQ ID NO 4668
; LENGTH: 164
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030237110A9 700455577H1
; LOCATION: 150
; OTHER INFORMATION: a, t, c, g, or other
US-09-923-876-4668
```

```
Query Match          15.8%; Score 24.4; DB 10; Length 164;
Best Local Similarity 60.6%; Pred. No. 4.4e+02;
Matches 40; Conservative 0; Mismatches 26; Indels 0; Gaps 0;
```

```
QY 68 GAGTCGGCGCGCCGCGACTCGACGATGAGCGAGATGACCACTCCGGCCGCGACTCGAC 127
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 139 GAGAGAGATGGCGAGGCGCGCGACAGAGATGCCCATCCGCTTCCGCATCGTC 80
QY 128 GATGAG 133
    ||| |||
Db 79 GTCGAG 74
```

```
RESULT 35
US-10-425-115-62701
; Sequence 62701, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 62701
; LENGTH: 183
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_157185C.1
US-10-425-115-62701
```

```
Query Match          15.8%; Score 24.4; DB 18; Length 183;
Best Local Similarity 56.1%; Pred. No. 4.4e+02;
Matches 46; Conservative 0; Mismatches 36; Indels 0; Gaps 0;
```

```
QY 47 CTGTCATCTCGTCATCTCGAGTCGGCGCGCGCGACTCGACGATGAGCGAGATGACC 106
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 19 CGGATCACTTGCTCAGCGCGAGCGCGAGCGGCAACGCCACGCAAGTGTCTGTCGC 78
QY 107 AGCTCCGCGCGCGCGACTCGACG 128
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

Db 79 ATCTACAGCCGGCGCTGAGG 100

RESULT 36

US-10-425-115-62701/c
; Sequence 62701, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 62701
; LENGTH: 183
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_157185C.1
US-10-425-115-62701

Query Match 15.8%; Score 24.4; DB 18; Length 183;
Best Local Similarity 56.1%; Pred. No. 4.4e+02;
Matches 46; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

Qy 27 CGTCGAGTCGGCGCCGCGAGCTGCTCATCTCGCTCATCGAGTCGGCGCCCGCGACT 86
Db 100 CCTCGACCGCCCGCGCTGTAGATGCCGACGAGCACCCTTGCGTGGCCGTTGCCCTCGGCT 41

Qy 87 CGACGATGAGCGAGATGACCAG 108
Db 40 CGCCGCTGAGCCAGGTGATCCG 19

RESULT 37

US-09-864-761-25686

; Sequence 25686, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annonmax Sequence Listing Engine vers. 1.1
; SEQ ID NO 25686
; LENGTH: 185
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AP000350.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 8.6
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 13
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 9.4
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 7.6
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 15
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 5.6
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 6.7
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 8.6
; OTHER INFORMATION: NT HIT: AF240786.1, EVALUATE 1.00e-100
; OTHER INFORMATION: SWISSPROT HIT: P30046, EVALUATE 8.00e-28
; OTHER INFORMATION: EST_HUMAN HIT: AV655183.1, EVALUATE 1.00e-100
US-09-864-761-25686

Query Match 15.8%; Score 24.4; DB 9; Length 185;
Best Local Similarity 53.5%; Pred. No. 4.4e+02;
Matches 76; Conservative 0; Mismatches 61; Indels 5; Gaps 1;

Qy 1 CGCCCGAGCTGTGTCATCTGCTCATCTGTCGAGTCGGCGGC-----CGAGCTGTGTCATC 55
Db 19 CGCCCGGCGCTGCGCATGCGCTGAGCGGGTCCACCGAGCCCTGCGCGAGCTGTGTCATC 78

Qy 56 TCCTCATCTGTCGAGTCGGCGCGCCCGCGACTGCAGATGAGCGAGATGACCACTCCGGC 115
Db 79 TCCTTCATCGCGGTAGTGGGCACCGCCGAGGACACCGCAGCCACAGCGCCCACTTCTTT 138

Qy 116 CGCCGACTCGACGATGAGCGAG 137
Db 139 GAGTTTCTCACCACGAGGACTAG 160

RESULT 38

US-09-864-761-25686/c

; Sequence 25686, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366

```
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 25686
; LENGTH: 185
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AP000350.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 8.6
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 13
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 9.4
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 7.6
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 15
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 5.6
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 6.7
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 8.6
; OTHER INFORMATION: NT HIT: AF240786.1, EVALUE 1.00e-100
; OTHER INFORMATION: SWISSPROT HIT: P30046, EVALUE 8.00e-28
; OTHER INFORMATION: EST_HUMAN HIT: AV655183.1, EVALUE 1.00e-100
; US-09-864-761-25686
```

```
Query Match 15.8%; Score 24.4; DB 9; Length 185;
Best Local Similarity 53.5%; Pred. No. 4.4e+02;
Matches 76; Conservative 0; Mismatches 61; Indels 5; Gaps 1;

QY 18 CTCGCTCATCGTCGAGTCGCGCGCGAGCTGTCATCTCGCTCATCGTCGAGTCGCGG 77
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 160 CTAGCTCCTGTGTGAGAACTCAAGAAGTGGCGCTGTGCTGCGTGTGCTCGCGG 101
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

QY 78 CCGCCGACTGCAGTGAAGCGAGATGACCACT-----CCGCGCGCGAGCTCGACGATGA 132
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 100 TGCCCACTACGCCGATGAGAGATGACAGCTGCGCGCAGGGGCTCGGTGACCCGCTCA 41
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

QY 133 GCGAGATGACCACTCCGCGG 154
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 40 GCGCCATGCCAGGCCCGCGG 19
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

RESULT 39
US-10-753-646-15
; Sequence 15, Application US/10753646
; Publication No. US20040138127A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Davidson, Donald J.
; TITLE OF INVENTION: NOVEL ANTIANGIOGENIC PEPTIDES,
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING SAME AND METHODS FOR INHIBITING
; TITLE OF INVENTION: ANGIOGENESIS
; FILE REFERENCE: 5940.US.P3
; CURRENT APPLICATION NUMBER: US/10/753,646
; CURRENT FILING DATE: 2004-01-08
; PRIOR APPLICATION NUMBER: US/08/924,287A
; PRIOR FILING DATE: 2004-01-08
; PRIOR APPLICATION NUMBER: US 08/851,350
; PRIOR FILING DATE: 1997-05-05
; PRIOR APPLICATION NUMBER: US 08/832,087
; PRIOR FILING DATE: 1997-04-03
; PRIOR APPLICATION NUMBER: US 08/643,219
; PRIOR FILING DATE: 1996-05-03
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 175
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic DNA Fragment synVB2
; US-10-753-646-15
```

```
Query Match 15.7%; Score 24.2; DB 18; Length 175;
Best Local Similarity 62.3%; Pred. No. 5.1e+02;
Matches 38; Conservative 0; Mismatches 23; Indels 0; Gaps 0;
```

```
QY 15 CATCTGCTCATCTGTCGAGTCGCGCGCGAGCTGTGTCATCTCGCTCATCTGAGTCGG 74
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 31 CATCAGGTGTGTGTCTGTGTCGCCGCGGACGCTGAAGAGCTGCTCACCCTCGGGTGG 90
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
```

```
QY 75 C 75
Db 91 C 91
```

```
RESULT 40
US-10-753-646-15/c
; Sequence 15, Application US/10753646
; Publication No. US20040138127A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Davidson, Donald J.
; TITLE OF INVENTION: NOVEL ANTIANGIOGENIC PEPTIDES,
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING SAME AND METHODS FOR INHIBITING
; TITLE OF INVENTION: ANGIOGENESIS
; FILE REFERENCE: 5940.US.P3
; CURRENT APPLICATION NUMBER: US/10/753,646
; CURRENT FILING DATE: 2004-01-08
; PRIOR APPLICATION NUMBER: US/08/924,287A
; PRIOR FILING DATE: 2004-01-08
; PRIOR APPLICATION NUMBER: US 08/851,350
; PRIOR FILING DATE: 1997-05-05
; PRIOR APPLICATION NUMBER: US 08/832,087
; PRIOR FILING DATE: 1997-04-03
; PRIOR APPLICATION NUMBER: US 08/643,219
; PRIOR FILING DATE: 1996-05-03
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 175
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic DNA Fragment synVB2
; US-10-753-646-15

Query Match 15.7%; Score 24.2; DB 18; Length 175;
Best Local Similarity 62.3%; Pred. No. 5.1e+02;
```


Matches 38; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 80 GCCGACTCGACGATGAGCGAGTACCGAGCTCCGCCCGGCGGACTCGACGATGAGCGAGAT 139

DB 91 GCCCACCAGAGGTGAGCGACGCTTTCAGCTGCCGCCGCGACACGACCAACCGGTGAT 32

QY 140 G 140

DB 31 G 31

RESULT 41

US-10-425-115-140476

; Sequence 140476, Application US/10425115

; Publication No. US20040214272A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.

; APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

; FILE REFERENCE: 38-21(53222)B

; CURRENT APPLICATION NUMBER: US/10/425,115

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 369326

; SEQ ID NO 140476

; LENGTH: 183

; TYPE: DNA

; ORGANISM: Zea mays

; FEATURE:

; NAME/KEY: unsure

; LOCATION: (1)..(183)

; OTHER INFORMATION: unsure at all n locations

; FEATURE:

; OTHER INFORMATION: Clone ID: MRT4577_59598C.1

; US-10-425-115-140476

Query Match 15.7%; Score 24.2; DB 18; Length 183;

Best Local Similarity 56.4%; Pred. No. 5e+02;

Matches 44; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 57 CGCTCATCTGTCGAGTCGGCGGCCCGGCGGACTCGACGATGAGCGAGATGACCGAGTCCGGCC 116

DB 4 CGACCATGGCCACCGGGGCGGACCAACCGCGGCGCATGGCTACCAACCGCGGCGGCG 63

QY 117 GCCGACTCGACGATGAGC 134

DB 64 TCCGACTCGCCGACGCGC 81

RESULT 42

US-10-425-115-140476/c

; Sequence 140476, Application US/10425115

; Publication No. US20040214272A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.

; APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

; FILE REFERENCE: 38-21(53222)B

; CURRENT APPLICATION NUMBER: US/10/425,115

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 369326

; SEQ ID NO 140476

; LENGTH: 183

; TYPE: DNA

; ORGANISM: Zea mays

; FEATURE:

; NAME/KEY: unsure

; LOCATION: (1)..(183)

; OTHER INFORMATION: unsure at all n locations

; FEATURE:

; OTHER INFORMATION: Clone ID: MRT4577_59598C.1

; US-10-425-115-140476

Query Match 15.7%; Score 24.2; DB 18; Length 183;

Best Local Similarity 56.4%; Pred. No. 5e+02;

Matches 44; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 21 GCTCATCTGTCGAGTCGGCGGCCCGGAGCTGTCATCTCGCTCATCTGAGTCGGCGGCCG 80

DB 81 GCGCGTCGCGGAGTCGAGCGCCGCGGCGGCTGTGTAGCCCATGCCGTGCGGTTGTGG 22

QY 81 CCGACTCGACGATGAGCG 98

DB 21 CCGCGGTGCGCATGTCG 4

RESULT 43

US-10-156-761-3130

; Sequence 3130, Application US/10156761

; Publication No. US20030119018A1

; GENERAL INFORMATION:

; APPLICANT: OMURA, SATOSHI

; APPLICANT: IKEDA, HARUO

; APPLICANT: ISHIKAWA, JUN

; APPLICANT: HORIKAWA, HIROSHI

; APPLICANT: SHIBA, TADAYOSHI

; APPLICANT: SAKAKI, YOSHIYUKI

; APPLICANT: HATTORI, MASAHIRA

; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES

; FILE REFERENCE: 249-262

; CURRENT APPLICATION NUMBER: US/10/156,761

; CURRENT FILING DATE: 2002-05-29

; PRIOR APPLICATION NUMBER: JP 2001-204089

; PRIOR FILING DATE: 2001-05-30

; PRIOR APPLICATION NUMBER: JP 2001-272697

; PRIOR FILING DATE: 2001-08-02

; NUMBER OF SEQ ID NOS: 15109

; SEQ ID NO 3130

; LENGTH: 192

; TYPE: DNA

; ORGANISM: Streptomyces avermitilis

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)..(192)

; US-10-156-761-3130

Query Match 15.3%; Score 23.6; DB 15; Length 192;

Best Local Similarity 64.8%; Pred. No. 7.7e+02;

Matches 35; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 54 TCTCGCTCATCTGTCGAGTCGGCGGCCCGGACTCGACGATGAGCGAGATGACCA 107

DB 104 TCGGTTCTATCTCGCGTCTCGACCGCTCGCCCGACCATCAACGAGCTGACGA 157

RESULT 44

US-10-156-761-3130/c

; Sequence 3130, Application US/10156761

; Publication No. US20030119018A1

; GENERAL INFORMATION:

; APPLICANT: OMURA, SATOSHI

; APPLICANT: IKEDA, HARUO

; APPLICANT: ISHIKAWA, JUN

; APPLICANT: HORIKAWA, HIROSHI

; APPLICANT: SHIBA, TADAYOSHI

; APPLICANT: SAKAKI, YOSHIYUKI

; APPLICANT: HATTORI, MASAHIRA

; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES

; FILE REFERENCE: 249-262

; CURRENT APPLICATION NUMBER: US/10/156,761

; CURRENT FILING DATE: 2002-05-29

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; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 3130
; LENGTH: 192
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(192)
US-10-156-761-3130

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Query Match          15.3%; Score 23.6; DB 15; Length 192;
Best Local Similarity 64.8%; Pred. No. 7.7e+02;
Matches 35; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

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OY      48 TGGTCATCTCGCTCATCGTCGAGTCGGCGCGCCGACTCGACGATGAGCGAGA 101
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DB      157 TCGTCAGCTCGTTGATGTGCGGGCGACGGTCGAGGACGAGATGAAACCGGA 104

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RESULT 45

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US-10-425-115-22757
; Sequence 22757, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 22757
; LENGTH: 155
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(155)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_120756C.1
US-10-425-115-22757

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Query Match          15.2%; Score 23.4; DB 18; Length 155;
Best Local Similarity 50.0%; Pred. No. 8.9e+02;
Matches 42; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

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OY      63 TCGTCGAGTCGGCGCGCCGACTCGACGATGAGCGAGATGACCACTCCGCGCCGAC 122
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB      57 TCGTCGACGGGGGGCGCGGCGAAGCAGCAGCTAAGNTNCAACCTCCNNCCGNTGAA 116

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OY      123 TCGACGATGAGCGAGATGACCAAGC 146
          ||||| ||||| ||||| |||||
DB      117 GCGACAGNGCCGAAGCGAGGAAC 140

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Search completed: April 9, 2005, 02:42:41
Job time : 498 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 9, 2005, 00:55:17 ; Search time 130 Seconds
(without alignments)
1938.359 Million cell updates/sec

Title: US-09-887-194A-13
Perfect score: 154
Sequence: 1 cggcgcgagctgctcatctc.....gagatgaccagctccgcccg 154

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 1407054

Minimum DB seq length: 0
Maximum DB seq length: 200

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Issued Patents NA: *
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq: *
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq: *
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq: *
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq: *
5: /cgn2_6/ptodata/1/ina/PTUS_COMB.seq: *
6: /cgn2_6/ptodata/1/ina/backfiles1.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28	18.2	197	4	US-09-313-294A-6653 Sequence 6653, Ap
2	28	18.2	197	4	US-09-313-294A-6653 Sequence 6653, Ap
3	26.6	17.3	195	4	US-09-513-999C-13979 Sequence 13979, A
4	26.6	17.3	195	4	US-09-513-999C-13979 Sequence 13979, A
5	26.2	17.0	171	4	US-09-621-976-19276 Sequence 19276, A
6	26.2	17.0	171	4	US-09-621-976-19276 Sequence 19276, A
7	25.6	16.6	183	3	US-08-952-670-3 Sequence 3, Appli
8	25.6	16.6	183	3	US-08-952-670-3 Sequence 3, Appli
9	25	16.2	123	3	US-09-247-190-34 Sequence 34, Appl
10	25	16.2	123	3	US-09-247-190-34 Sequence 34, Appl
11	24.8	16.1	181	4	US-09-513-999C-16612 Sequence 16612, A
12	24.8	16.1	181	4	US-09-513-999C-16612 Sequence 16612, A
13	24.2	15.7	175	3	US-08-851-350-15 Sequence 15, Appl
14	24.2	15.7	175	3	US-08-851-350-15 Sequence 15, Appl
15	24.2	15.7	175	4	US-08-924-287A-15 Sequence 15, Appl
16	24.2	15.7	175	4	US-08-924-287A-15 Sequence 15, Appl
17	23.6	15.3	71	4	US-09-513-999C-15749 Sequence 15749, A
18	23.6	15.3	71	4	US-09-513-999C-15749 Sequence 15749, A
19	23.6	15.3	195	4	US-09-902-540-8568 Sequence 8568, Ap
20	23.6	15.3	195	4	US-09-902-540-8568 Sequence 8568, Ap
21	23.2	15.1	126	4	US-09-902-540-2996 Sequence 2996, Ap
22	23.2	15.1	126	4	US-09-902-540-2996 Sequence 2996, Ap
23	22.6	14.7	185	3	US-08-447-985-14 Sequence 14, Appl
24	22.6	14.7	185	3	US-08-447-985-14 Sequence 14, Appl
25	22.6	14.7	185	4	US-08-852-340-14 Sequence 14, Appl
26	22.6	14.7	185	4	US-08-852-340-14 Sequence 14, Appl
27	22.6	14.7	195	2	US-08-622-740-9 Sequence 9, Appli

C 28	22.6	14.7	195	2	US-08-622-740-9	Sequence 9, Appli
C 29	22.6	14.7	195	3	US-08-440-689-9	Sequence 9, Appli
C 30	22.6	14.7	195	3	US-08-440-689-9	Sequence 9, Appli
C 31	22.6	14.7	195	3	US-09-122-399-9	Sequence 9, Appli
C 32	22.6	14.7	195	3	US-09-122-399-9	Sequence 9, Appli
C 33	22.6	14.7	195	4	US-08-440-646A-9	Sequence 9, Appli
C 34	22.6	14.7	195	4	US-08-440-646A-9	Sequence 9, Appli
C 35	22.6	14.7	200	1	US-08-105-168B-6	Sequence 6, Appli
C 36	22.6	14.7	200	1	US-08-105-168B-6	Sequence 6, Appli
C 37	22.6	14.7	200	2	US-08-698-948-6	Sequence 6, Appli
C 38	22.6	14.7	200	2	US-08-698-948-6	Sequence 6, Appli
C 39	22.4	14.5	174	4	US-09-902-540-8045	Sequence 8045, Ap
C 40	22.4	14.5	174	4	US-09-902-540-8045	Sequence 8045, Ap
C 41	22	14.3	102	4	US-09-902-540-7303	Sequence 7303, Ap
C 42	22	14.3	102	4	US-09-902-540-7303	Sequence 7303, Ap
C 43	22	14.3	164	4	US-09-313-294A-6924	Sequence 6924, Ap
C 44	22	14.3	164	4	US-09-313-294A-6924	Sequence 6924, Ap
C 45	22	14.3	180	4	US-09-902-540-8725	Sequence 8725, Ap
C 46	22	14.3	180	4	US-09-902-540-8725	Sequence 8725, Ap
C 47	22	14.3	195	6	5212296-18	Patent No. 5212296
C 48	22	14.3	195	6	5212296-18	Patent No. 5212296
C 49	22	14.3	195	6	5212296-18	Patent No. 5212296
C 50	22	14.3	195	6	5212296-18	Patent No. 5212296
C 51	21.8	14.2	192	4	US-09-902-540-5945	Sequence 5945, Ap
C 52	21.8	14.2	192	4	US-09-902-540-5945	Sequence 5945, Ap
C 53	21.6	14.0	141	4	US-09-513-999C-34193	Sequence 34193, A
C 54	21.6	14.0	141	4	US-09-513-999C-34193	Sequence 34193, A
C 55	21.6	14.0	165	4	US-09-313-294A-3879	Sequence 3879, Ap
C 56	21.6	14.0	165	4	US-09-313-294A-3879	Sequence 3879, Ap
C 57	21.6	14.0	169	3	US-09-060-756-698	Sequence 698, App
C 58	21.6	14.0	169	3	US-09-060-756-698	Sequence 698, App
C 59	21.6	14.0	169	4	US-09-670-314-698	Sequence 698, App
C 60	21.6	14.0	169	4	US-09-670-314-698	Sequence 698, App
C 61	21.4	13.9	106	4	US-09-513-999C-14237	Sequence 14237, A
C 62	21.4	13.9	106	4	US-09-513-999C-14237	Sequence 14237, A
C 63	21.4	13.9	145	4	US-09-513-999C-16999	Sequence 16999, A
C 64	21.4	13.9	145	4	US-09-513-999C-16999	Sequence 16999, A
C 65	21.4	13.9	158	4	US-09-313-294A-719	Sequence 719, App
C 66	21.4	13.9	158	4	US-09-313-294A-719	Sequence 719, App
C 67	21.4	13.9	189	4	US-09-902-540-2496	Sequence 2496, Ap
C 68	21.4	13.9	189	4	US-09-902-540-2496	Sequence 2496, Ap
C 69	21.4	13.9	189	4	US-09-902-540-7545	Sequence 7545, Ap
C 70	21.4	13.9	189	4	US-09-902-540-7545	Sequence 7545, Ap
C 71	21.2	13.8	146	4	US-09-270-767-29054	Sequence 29054, A
C 72	21.2	13.8	146	4	US-09-270-767-29054	Sequence 29054, A
C 73	21.2	13.8	174	4	US-09-902-540-2977	Sequence 2977, Ap
C 74	21.2	13.8	174	4	US-09-902-540-2977	Sequence 2977, Ap
C 75	21.2	13.8	192	4	US-09-513-999C-21223	Sequence 21223, A
C 76	21.2	13.8	192	4	US-09-513-999C-21223	Sequence 21223, A
C 77	21	13.6	45	4	US-08-899-112B-21	Sequence 21, Appl
C 78	21	13.6	45	4	US-08-899-112B-21	Sequence 21, Appl
C 79	21	13.6	45	4	US-09-011-553-22	Sequence 22, Appl
C 80	21	13.6	45	4	US-09-011-553-22	Sequence 22, Appl
C 81	21	13.6	135	4	US-09-902-540-7592	Sequence 7592, Ap
C 82	21	13.6	135	4	US-09-902-540-7592	Sequence 7592, Ap
C 83	21	13.6	153	4	US-09-902-540-9430	Sequence 9430, Ap
C 84	21	13.6	153	4	US-09-902-540-9430	Sequence 9430, Ap
C 85	21	13.6	156	4	US-09-902-540-5903	Sequence 5903, Ap
C 86	21	13.6	156	4	US-09-902-540-5903	Sequence 5903, Ap
C 87	21	13.6	199	4	US-09-719-108-4	Sequence 4, Appli
C 88	21	13.6	199	4	US-09-719-108-4	Sequence 4, Appli
C 89	20.8	13.5	124	4	US-09-902-540-4184	Sequence 4184, Ap
C 90	20.8	13.5	124	4	US-09-902-540-4184	Sequence 4184, Ap
C 91	20.8	13.5	156	4	US-09-313-294A-4707	Sequence 4707, Ap
C 92	20.8	13.5	156	4	US-09-313-294A-4707	Sequence 4707, Ap
C 93	20.8	13.5	171	4	US-09-313-294A-3925	Sequence 3925, Ap
C 94	20.8	13.5	171	4	US-09-313-294A-3925	Sequence 3925, Ap
C 95	20.8	13.5	174	3	US-09-017-631-26	Sequence 26, Appl
C 96	20.8	13.5	174	3	US-09-017-631-26	Sequence 26, Appl
C 97	20.8	13.5	174	3	US-09-018-138-4	Sequence 4, Appli
C 98	20.8	13.5	174	3	US-09-018-138-4	Sequence 4, Appli
C 99	20.8	13.5	177	4	US-09-902-540-2860	Sequence 2860, Ap
C 100	20.8	13.5	177	4	US-09-902-540-2860	Sequence 2860, Ap

APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
Patent No. 6783961
FILE REFERENCE: 59.US2.REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 13979
LENGTH: 195
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: 9
OTHER INFORMATION: s=g or c
FEATURE:
NAME/KEY: misc_feature
LOCATION: 11
OTHER INFORMATION: n=a, g, c or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: 57
OTHER INFORMATION: r=a or g
US-09-513-999C-13979

Query Match 17.3%; Score 26.6; DB 4; Length 195;
Best Local Similarity 56.2%; Pred. No. 4.5e+02;
Matches 50; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

QY 30 CGAGTCGGCGCCGGAGCTGTCATCTCGCTCATCTCGAGTCGGCGCCCGGCGACTCGA 89
DB 134 CGAGCCGGCGGCTGAGCTGGGAGCTAGACCTAGCGCCGAGCGAAGAAATCC 75
QY 90 CGATGAGCGAGATGACCACTCCGCGCC 118
DB 74 CGCCGACGCGAGACACACGCGCCGACG 46

RESULT 5
US-09-621-976-19276
Sequence 19276, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTs and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 19276
LENGTH: 171
TYPE: DNA
ORGANISM: Homo sapiens
US-09-621-976-19276

Query Match 17.0%; Score 26.2; DB 4; Length 171;
Best Local Similarity 55.1%; Pred. No. 5.7e+02;
Matches 49; Conservative 1; Mismatches 39; Indels 0; Gaps 0;

QY 37 GCGCGGAGCTGTCATCTCGCTCATCTCGAGTCGGCGCCCGGCGACTCGAGATGAG 96
DB 47 GCTGCGGCGGCGGTGTCTCGCGTTCCGCGGAGATTCTCTTCGCTCCGCTCGGCTAGGT 106
QY 97 CGAGATGACCACTCCGCGCCGCGACTCG 125
DB 107 CTACGTCCCACTCAGCCGCGCGMTCC 135

RESULT 6
US-09-621-976-19276/c
Sequence 19276, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTs and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 19276
LENGTH: 171
TYPE: DNA
ORGANISM: Homo sapiens
US-09-621-976-19276

Query Match 17.0%; Score 26.2; DB 4; Length 171;
Best Local Similarity 55.1%; Pred. No. 5.7e+02;
Matches 49; Conservative 1; Mismatches 39; Indels 0; Gaps 0;

QY 30 CGAGTCGGCGCCGGAGCTGTCATCTCGCTCATCTCGAGTCGGCGCCCGGCGACTCGA 89
DB 135 CGAKCCGGCGGCTGAGCTGGGAGCTAGACCTAGCGCCGAGCGAAGAAATCC 76
QY 90 CGATGAGCGAGATGACCACTCCGCGCC 118
DB 75 CGCCGACGCGAGACACCGCGCCGACG 47

RESULT 7
US-08-952-670-3
Sequence 3, Application US/08952670
Patent No. 6117636
GENERAL INFORMATION:
APPLICANT: Taddai, Emmanuelle
APPLICANT: Aufere, Robert
TITLE OF INVENTION: METHOD FOR DETECTING HEAT-RESISTANT
TITLE OF INVENTION: MICRO-ORGANISMS CAPABLE OF CONTAMINATING CERTAIN FOOD
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/952,670
FILING DATE: 09-MAR-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR96/00821
FILING DATE: 31-MAY-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 95/06578
FILING DATE: 02-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Granados, Patricia D.
REGISTRATION NUMBER: 33,683
REFERENCE/DOCKET NUMBER: 065691/0128
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300

TELEFAX: (202) 672-5399
 TELEEX: 904136
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 183 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 US-08-952-670-3

Query Match 16.6%; Score 25.6; DB 3; Length 183;
 Best Local Similarity 59.7%; Pred. No. 8e+02;
 Matches 43; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 64 CGTCGAGTCGGCGCGCCGAGCTGACGATGAGGAGATGACGCTCCGCGCGGACT 123
 DB 67 CGCGGTTTCGACGCGCGCGCGGAGGCTTCGCGCGCGCGCGCGCGGAGAGACC 126
 QY 124 CGACGATGAGCG 135
 DB 127 CCAACATGACG 138

RESULT 8

US-08-952-670-3/c
 Sequence 3, Application US/08952670
 Patent No. 6117636

GENERAL INFORMATION:
 APPLICANT: Tadei, Emmanuelle
 APPLICANT: Aufreere, Robert
 TITLE OF INVENTION: METHOD FOR DETECTING HEAT-RESISTANT
 TITLE OF INVENTION: MICRO-ORGANISMS CAPABLE OF CONTAMINATING CERTAIN FOOD
 TITLE OF INVENTION: PRODUCTS
 NUMBER OF SEQUENCES: 12
 CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley & Lardner
 STREET: 3000 K Street, N.W., Suite 500
 CITY: Washington
 STATE: D.C.

COUNTRY: USA
 ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/952,670
 FILING DATE: 09-MAR-1998

CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/FR96/00821
 FILING DATE: 31-MAY-1996

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: FR 95/06578
 FILING DATE: 02-JUN-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Granados, Patricia D.
 REGISTRATION NUMBER: 33,683
 REFERENCE/DOCKET NUMBER: 065691/0128

TELEPHONE: (202) 672-5300
 TELEFAX: (202) 672-5399
 TELEEX: 904136

INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 183 base pairs
 TYPE: nucleic acid

STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 US-08-952-670-3

Query Match 16.6%; Score 25.6; DB 3; Length 183;
 Best Local Similarity 59.7%; Pred. No. 8e+02;
 Matches 43; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 20 CGTCATGCTGAGTCGGCGCGGAGCTGTGATCTGCTCATCTGAGTCGCGCGG 79
 DB 138 CGTTCATGTTGGGTCTTCGCGCGGCGCGCGCGCGCGCGCGAGGCTCCCGCGCGG 79
 QY 80 GCCGACTGACG 91
 DB 78 GTGAAACGCG 67

RESULT 9

US-09-247-190-34
 Sequence 34, Application US/09247190
 Patent No. 6261804

GENERAL INFORMATION:
 APPLICANT: Szostak, Jack W.
 APPLICANT: Roberts, Richard W.
 APPLICANT: Liu, Rihe
 TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
 TITLE OF INVENTION: FUSIONS
 FILE REFERENCE: 00786/350005
 CURRENT APPLICATION NUMBER: US/09/247,190
 CURRENT FILING DATE: 1999-02-09

EARLIER APPLICATION NUMBER: 60/035,963
 EARLIER FILING DATE: 1997-01-21
 EARLIER APPLICATION NUMBER: 60/064,491
 EARLIER FILING DATE: 1997-11-06
 EARLIER APPLICATION NUMBER: 09/007,005
 EARLIER FILING DATE: 1998-01-14

NUMBER OF SEQ ID NOS: 38
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 34

LENGTH: 123
 TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

OTHER INFORMATION: n = a, g, t, or c. s = c or g.
 US-09-247-190-34

Query Match 16.2%; Score 25; DB 3; Length 123;
 Best Local Similarity 15.0%; Pred. No. 1.1e+03;
 Matches 16; Conservative 26; Mismatches 65; Indels 0; Gaps 0;

QY 18 CTCGCTCATGCTGAGTCGGCGCGGAGCTGTGATCTGCTCATCTGAGTCGCGG 77
 DB 12 CTTGTGATCTGCTGAGTCGGCGCGGAGCTGTGATCTGCTCATCTGAGTCGCGG 71
 QY 78 CCGCGACTGACGATGAGGAGATGACGAGCTCCGCGCGGACTC 124
 DB 72 NSNNSNNSNNSNNSNNSNNSNNSNNSNNSNNSNNSNNSNNSNNSN 118

RESULT 10

US-09-247-190-34/c
 Sequence 34, Application US/09247190
 Patent No. 6261804

GENERAL INFORMATION:
 APPLICANT: Szostak, Jack W.
 APPLICANT: Roberts, Richard W.
 APPLICANT: Liu, Rihe

TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
 TITLE OF INVENTION: FUSIONS
 FILE REFERENCE: 00786/350005
 CURRENT APPLICATION NUMBER: US/09/247,190
 CURRENT FILING DATE: 1999-02-09

EARLIER APPLICATION NUMBER: 60/035,963
 EARLIER FILING DATE: 1997-01-21
 EARLIER APPLICATION NUMBER: 60/064,491
 EARLIER FILING DATE: 1997-11-06

```
; EARLIER APPLICATION NUMBER: 09/007,005
; EARLIER FILING DATE: 1998-01-14
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 123
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: n = a, g, t, or c. s = c or g.
US-09-247-190-34

Query Match          16.2%; Score 25; DB 3; Length 123;
Best Local Similarity 15.0%; Pred. No. 1.1e+03;
Matches 16; Conservative 26; Mismatches 65; Indels 0; Gaps 0;

Qy      31 GAGTCGCGCGCCGAGCTGTCATCTCGCTCATCTCGAGTCGGCGCCGCGACTCGAC 90
      ||| ||| ||| ||| : : : : : : : : : : : : : : : : : :
Db      118 GAGCAAGGCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 59
      : : : : : : : : : : : : : : : : : : : : : : :

Qy      91 GATGAGCGAGATGACCACTCCGCGCGCGCGACTCGACGATGAGCGAG 137
      : : : : : : : : : : : : : : : : : : : : : : :
Db      58 SNNNSNNNSNNNSNNNSNNNSNNNSNNNSNNNSNNNSNNNSNNNSNNNSNNNSNN 12
      : : : : : : : : : : : : : : : : : : : : : : :

RESULT 11
US-09-513-999C-16612
; Sequence 16612, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 16612
; LENGTH: 181
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-513-999C-16612

Query Match          16.1%; Score 24.8; DB 4; Length 181;
Best Local Similarity 67.3%; Pred. No. 1.3e+03;
Matches 35; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

Qy      25 ATCGTCAGTCGCGCGCGCGAGCTGTCATCTCGCTCATCTCGAGTCGCGG 76
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      20 ATCCCTACTCTGCGGCGCGCGAGCGCTGTGCTTTCGCGCGCGCGCG 71
      : : : : : : : : : : : : : : : : : : : : : : :

RESULT 12
US-09-513-999C-16612/c
; Sequence 16612, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
```

```
; SOFTWARE: Patent.pm
; SEQ ID NO 16612
; LENGTH: 181
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-513-999C-16612

Query Match          16.1%; Score 24.8; DB 4; Length 181;
Best Local Similarity 67.3%; Pred. No. 1.3e+03;
Matches 35; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

Qy      79 CGCCGACTCGACGATGAGCGAGATGACCACTCCGCGCCGCGACTCGACGAT 130
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      71 CGCCGCGCGCGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 20
      : : : : : : : : : : : : : : : : : : : : : : :

RESULT 13
US-08-851-350-15
; Sequence 15, Application US/08851350
; Patent No. 6057122
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; TITLE OF INVENTION: NOVEL ANTIANGIOGENIC PEPTIDES,
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING SAME AND METHODS
; TITLE OF INVENTION: FOR INHIBITING ANGIOGENESIS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/851,350
; FILING DATE: 05-MAY-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Casuto, Dianne
; REGISTRATION NUMBER: 40,943
; REFERENCE/DOCKET NUMBER: 5940.US.P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847-938-3137
; TELEFAX: 847-938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 175 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-851-350-15

Query Match          15.7%; Score 24.2; DB 3; Length 175;
Best Local Similarity 62.3%; Pred. No. 1.8e+03;
Matches 38; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

Qy      15 CATCTGCTCATCTGTCGAGTCGGCGCGAGCTGTCATCTCGCTCATCTGAGTCGG 74
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      31 CATCAGGTGTGTGTGTGTCGCGCGCGCGAGCTGAAGAGTGGCTCACCTTCGGGTGG 90
      : : : : : : : : : : : : : : : : : : : : : : :

Qy      75 C 75
      |
Db      91 C 91
```

```

RESULT 14
US-08-851-350-15/c
; Sequence 15, Application US/08851350
; Patent No. 6057122
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; TITLE OF INVENTION: NOVEL ANTIANGIOGENIC PEPTIDES,
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING SAME AND METHODS
; TITLE OF INVENTION: FOR INHIBITING ANGIOGENESIS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/851,350
; FILING DATE: 05-MAY-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Casuto, Dianne
; REGISTRATION NUMBER: 40,943
; REFERENCE/DOCKET NUMBER: 5940.US.P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847-938-3137
; TELEFAX: 847-938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 175 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-851-350-15

Query Match      15.7%; Score 24.2; DB 3; Length 175;
Best Local Similarity 62.3%; Pred. No. 1.8e+03;
Matches 38; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY      80 GCCGACTCGACGATGAGCGGAGATGACCAGCTCCGCCGCCGAGCTCGACGATGAGCGAGAT 139
       ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      91 GCCCACC CGAAGGTGAGCCAGCTCTTCAGTGC CGCGGACACCA CCACCGTGAT 32
       ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY      140 G 140
       |
Db      31 G 31

RESULT 15
US-08-924-287A-15
; Sequence 15, Application US/08924287A
; Patent No. 6699838
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Davidson, Donald J.
; TITLE OF INVENTION: NOVEL ANTIANGIOGENIC PEPTIDES,
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING SAME AND METHODS FOR INHIBITING
; TITLE OF INVENTION: ANGIOGENESIS
; FILE REFERENCE: 5940.US.P3
; CURRENT APPLICATION NUMBER: US/08/924,287A
; CURRENT FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: US 08/851,350

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; PRIOR FILING DATE: 1997-05-05
; PRIOR APPLICATION NUMBER: US 08/832,087
; PRIOR FILING DATE: 1997-04-03
; PRIOR APPLICATION NUMBER: US 08/643,219
; PRIOR FILING DATE: 1996-05-03
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 175
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic DNA Fragment synVB2
US-08-924-287A-15

Query Match          15.7%; Score 24.2; DB 4; Length 175;
Best Local Similarity 62.3%; Pred. No. 1.8e+03;
Matches 38; Conservative 0; Mismatches 23; Indels 0; Gaps 0,

QY      15 CATTCGCTCATCGTCGAGTCGCGCCGCGGAGCTGTCATCTCGCTCATCGTCGAGTCGG 74
      ||||| ||| | ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      31 CATCACGGTGTGTCGTGTGTCGCCGCCGCGCAGCTGAAGAGCTGTGCTCACCTTCGGGTGG 90

QY      75 C 75
      |
Db      91 C 91

```

```

RESULT 16
US-08-924-287A-15/c
; Sequence 15, Application US/08924287A
; Patent No. 6699838
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Davidson, Donald J.
; TITLE OF INVENTION: NOVEL ANTIANGIOGENIC PEPTIDES,
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING SAME, AND METHODS FOR INHIBITING
; TITLE OF INVENTION: ANGIOGENESIS
; FILE REFERENCE: 5940.US.P3
; CURRENT APPLICATION NUMBER: US/08/924,287A
; CURRENT FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: US 08/851,350
; PRIOR FILING DATE: 1997-05-05
; PRIOR APPLICATION NUMBER: US 08/832,087
; PRIOR FILING DATE: 1997-04-03
; PRIOR APPLICATION NUMBER: US 08/643,219
; PRIOR FILING DATE: 1996-05-03
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 175
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic DNA Fragment synVB2
US-08-924-287A-15

Query Match      15.7%; Score 24.2; DB 4; Length 175;
Best Local Similarity 62.3%; Pred. No. 1.8e+03;
Matches 38; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY      80 GCCGACTGACGATGAGCGAGATGACCACTCCGGCGCCGACTCGACGATGACGAGAT 139
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      91 GCCACCCGGAAGGTGAGCCAGCTCTTCACTGCGCGCGGACACGAGACCACCGTGTAT 32

QY      140 G 140
      |
Db      31 G 31

RESULT 17
US-09-513-999C-15749
; Sequence 15749, Application US/09513999C

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```
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 15749
; LENGTH: 71
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 35
; OTHER INFORMATION: r=a or g
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 45
; OTHER INFORMATION: s=g or c
; US-09-513-999C-15749
```

```
Query Match          15.3%; Score 23.6; DB 4; Length 71;
Best Local Similarity 62.5%; Pred. No. 2.4e+03;
Matches 35; Conservative 1; Mismatches 20; Indels 0; Gaps 0;
```

```
OY 73 GCGCGCGCGCGACTCGACGATGAGCGAGATGACCGCTCCGCCGCCGACTCGACG 128
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 8  GCGCGCGCGCGGTGACGCGCGCGCGCGACCCGASCCAGCGCGGACAGACG 63
```

RESULT 18

```
US-09-513-999C-15749/c
; Sequence 15749, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 15749
; LENGTH: 71
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 35
; OTHER INFORMATION: r=a or g
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 45
; OTHER INFORMATION: s=g or c
; US-09-513-999C-15749
```

```
Query Match          15.3%; Score 23.6; DB 4; Length 71;
Best Local Similarity 62.5%; Pred. No. 2.4e+03;
Matches 35; Conservative 1; Mismatches 20; Indels 0; Gaps 0;
```

```
OY 27 CGTCGAGTCGCGCGCGCGAGGCTGTCATCTCGCTCATGTCGAGTCGCGCGCGCC 82
```

```
DB 63 CGTCCTGTCCCGCGCTGCGTGGGTCTTTCGCGCGCGCGCTCCACCGCGCGCGCC 8
```

```
RESULT 19
US-09-902-540-8568
; Sequence 8568, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 8568
; LENGTH: 195
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
; US-09-902-540-8568
```

```
Query Match          15.3%; Score 23.6; DB 4; Length 195;
Best Local Similarity 58.6%; Pred. No. 2.5e+03;
Matches 41; Conservative 0; Mismatches 29; Indels 0; Gaps 0;
```

```
OY 9  GCTGTATCTCTGCTCATGTCGAGTCGCGCGCGCGAGCTGTCTATCTCGCTATCTCG 68
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 93 GCTGCGGTGCGGTGTCGACGACGCGAGGCGCGGACGCGCGCAAGCGCGCTCCGCG 152
```

```
OY 69 AGTCGCGGC 78
      ||||| |||||
DB 153 GCTCGCGCC 162
```

RESULT 20

```
US-09-902-540-8568/c
; Sequence 8568, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 8568
; LENGTH: 195
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
; US-09-902-540-8568
```

```
Query Match          15.3%; Score 23.6; DB 4; Length 195;
Best Local Similarity 58.6%; Pred. No. 2.5e+03;
Matches 41; Conservative 0; Mismatches 29; Indels 0; Gaps 0;
```

```
OY 77 GCGCGCGACTCGACGATGAGCGAGATGACCGCTCCGCCGCCGACTCGACGATGACGA 136
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 162 GCGCGCGCGCGCGCGCGCGCGCGCTTGGCGCGCGCTCCGCGCGCTCGACCGC 103
```

```
OY 137 GATGACGAC 146
      ||||| |||||
DB 102 GACCGCCAGC 93
```


Matches 43; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 27 CGTCGAGTCGGCGCGGAGCTGTGTCATCGCTCATGTCGAGTCGGCGCGCGCGGACT 86
Db 126 CGACGGGAGAGCTGGCGGTGACTTGAGCCCTGGAACGAGCGAGCGGCGGTGCGGACG 67

QY 87 CGACGATGAGCGAGATG 103
Db 66 AGCCATCATCAGGTG 50

RESULT 27

US-08-622-740-9

; Sequence 9, Application US/08622740
; Patent No. 5990390

; GENERAL INFORMATION:

; APPLICANT: Lundquist, Ronald C.

; APPLICANT: Walters, David A.

; APPLICANT: Kirihara, Julie A.

; TITLE OF INVENTION: Methods and Compositions for the
; TITLE OF INVENTION: Production of Stably Transformed, Fertile Monocot Plants

; NUMBER OF SEQUENCES: 22

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth, P.A.

; STREET: 3500 IDS Center

; CITY: Minneapolis

; STATE: MN

; COUNTRY: USA

; ZIP: 55402

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/622,740

; FILING DATE: 27-MARCH-1996

; CLASSIFICATION: 800

; ATTORNEY/AGENT INFORMATION:

; NAME: Woessner, Warren D.

; REGISTRATION NUMBER: 30,440

; REFERENCE/DOCKET NUMBER: 950.013US4

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 612-339-0331

; TELEFAX: 612-339-3061

; INFORMATION FOR SEQ ID NO: 9:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 195 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

US-08-622-740-9

Query Match 14.7%; Score 22.6; DB 2; Length 195;
Best Local Similarity 52.7%; Pred. No. 4.5e+03;

Matches 49; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY 36 GCGCGCGGAGCTGTGTCATCGCTCATGTCGAGTCGGCGCGCGCGGACTGACGATGA 95
Db 44 GCGCGCGGAGCTGTGTCATCGCTCATGTCGAGTCGGCGCGCGCGGACTGACGATGA 103

QY 96 GCGAGATGACGAGCTCCGCGCGCGGAGCTGACG 128
Db 104 AGGGGCTCAAGTCACCGCGGAGCTCCCGGTG 136

RESULT 28

US-08-622-740-9/c

; Sequence 9, Application US/08622740
; Patent No. 5990390

; GENERAL INFORMATION:

; APPLICANT: Lundquist, Ronald C.

; APPLICANT: Walters, David A.

; TITLE OF INVENTION: Methods and Compositions for the
; TITLE OF INVENTION: Production of Stably Transformed, Fertile Monocot Plants

; NUMBER OF SEQUENCES: 22

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth, P.A.

; STREET: 3500 IDS Center

; CITY: Minneapolis

; STATE: MN

; COUNTRY: USA

; ZIP: 55402

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/622,740

; FILING DATE: 27-MARCH-1996

; CLASSIFICATION: 800

; ATTORNEY/AGENT INFORMATION:

; NAME: Woessner, Warren D.

; REGISTRATION NUMBER: 30,440

; REFERENCE/DOCKET NUMBER: 950.013US4

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 612-339-0331

; TELEFAX: 612-339-3061

; INFORMATION FOR SEQ ID NO: 9:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 195 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

US-08-622-740-9

Query Match 14.7%; Score 22.6; DB 2; Length 195;
Best Local Similarity 52.7%; Pred. No. 4.5e+03;

Matches 49; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY 27 CGTCGAGTCGGCGCGGAGCTGTGTCATCGCTCATGTCGAGTCGGCGCGCGCGGACT 86
Db 136 CGACGGGAGAGCTGGCGGTGACTTGAGCCCTGGAACGAGCGAGCGGCGGTGCGGACG 77

QY 87 CGACGATGAGCGAGATGACCGAGCTCCGCGCGCC 119
Db 76 AGCCATCATCAGGTGTCATCAGGTGCGCGCC 44

RESULT 29

US-08-440-689-9

; Sequence 9, Application US/08440689
; Patent No. 6025545

; GENERAL INFORMATION:

; APPLICANT: Lundquist, Ronald C.

; APPLICANT: Walters, David A.

; APPLICANT: Kirihara, Julie A.

; TITLE OF INVENTION: Methods and Compositions for the
; TITLE OF INVENTION: Production of Stably Transformed, Fertile Monocot Plants

; NUMBER OF SEQUENCES: 22

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth, P.A.

; STREET: 3500 IDS Center

; CITY: Minneapolis

; STATE: MN

; COUNTRY: USA

; ZIP: 55402

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS


```

1  APPLICATION NUMBER: US/08/440,646A
2  FILING DATE: 15-May-1995
3  CLASSIFICATION: 800
4
5  PRIOR APPLICATION DATA:
6  APPLICATION NUMBER: US/08/112,245
7  FILING DATE: 25-AUG-1993
8
9  ATTORNEY/AGENT INFORMATION:
10 NAME: Woessner, Warren D.
11 REGISTRATION NUMBER: 30,440
12 REFERENCE/DOCKET NUMBER: 950.13US01
13
14 TELECOMMUNICATION INFORMATION:
15 TELEPHONE: 612-339-0331
16 TELEFAX: 612-339-3061
17
18 INFORMATION FOR SEQ ID NO: 9:
19
20 SEQUENCE CHARACTERISTICS:
21 LENGTH: 195 base pairs
22 TYPE: nucleic acid
23 STRANDEDNESS: single
24 TOPOLOGY: linear
25
26 SEQUENCE DESCRIPTION: SEQ ID NO: 9:
27
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31
32
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Query Match	14.7%;	Score 22.6;	DB 4;	Length 195;
Best Local Similarity	52.7%;	Pred. No. 4.5e+03;		
Matches 49; Conservative	0;	Mismatches 44;	Indels 0;	Gaps 0;

Oy 27 CGTCAGTCCGCGGCCGAGCTGTGCATCTCGCTCAGTCCGCGGCCGACT 86
 ||| | | | | | | | | | | | | | | | | | | | | |
Db 136 CGACGGGAGGCTGCGCGTGCACTTAGAGCCCCGTGGAACGAGCCGACGGCGGTGGCTGACG 77

Qy 87 CGACGATGAGCGAGATGACCAAGCTCCGGCCGC 119
| | | | | | | | | | | | | | | | | | | | | |
Db 76 AGGCCATCATCACGGTTATCATCAGGTGGGCGCC 44

RESULT 35
 US-08-105-168B-6
 ; Sequence 6, Application US/08105168B
 ; Patent No. 5589585
 ; GENERAL INFORMATION:
 ; APPLICANT: MABILAT et al.
 ; TITLE OF INVENTION: DNA FRAGMENTS OF MYCOBACTERIA, AMPLIFICATION
 ; TITLE OF INVENTION: PRIMERS, HYBRIDIZATION PROBES, REAGENTS AND METHOD FOR THE DET
 ; TITLE OF INVENTION: MYCOBACTERIA
 ; NUMBER OF SEQUENCES: 23
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Oliff & Berridge
 ; STREET: 700 South Washington Street, Suite 300
 ; CITY: Alexandria,
 ; STATE: Virginia
 ; ZIP: 22314
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5" DS/HD
 ; COMPUTER: IBM compatible
 ; OPERATING SYSTEM: MS DOS 3.1
 ; SOFTWARE: Wordperfect
 ; CURRENT APPLICATION DATA:
 ; FILING DATE: August 12, 1993
 ; APPLICATION NUMBER: US/08/105,168B
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: FR9210094
 ; FILING DATE: August 8, 1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: William P. Berridge
 ; REGISTRATION NUMBER: 30,024
 ; REFERENCE/DOCKET NUMBER: WPB 28835
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (703) 836-6400
 ; TELEFAX: (703) 836-2787
 ; INFORMATION FOR SEQ ID NO: 6:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 200 base pairs

```

? TYPE: nucleic acid
? STRANDEDNESS: single-stranded
? TOPOLOGY: linear
? MOLECULE TYPE: DNA (genomic)
? HYPOTHETICAL:
? ANTI-SENSE:
? ORIGINAL SOURCE:
? ORGANISM: Mycobacterium intracellulare
? STRAIN:
? INDIVIDUAL ISOLATE:
? POSITION IN GENOME:
? CHROMOSOME/SEGMENT:
? MAP POSITION:
? FEATURE:
? NAME/KEY:
? LOCATION: 518-717
? IDENTIFICATION METHOD:
? OTHER INFORMATION:
US-08-105-168B-6

```

Query Match	14.78;	Score 22.6;	DB 1;	Length 200;
Best Local Similarity	57.18;	Pred. No. 4.5e+03;		
Matches 60; Conservative	0;	Mismatches 44;	Indels 1;	Gaps 1;

Oy 9 GCTGGTATCTCGCTCATCTCGAGTGGCGGCCGAGCTGTCATCTCGCTCATCGTCG 68
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 70 GCTGGGTCCAAGCGCGGCATCCGAGAAGGCCGTC-GAGAAGTCAACCGAGACCCCTGCTCA 128

Qy	69	AGTCGGCGCGCCGACTCGACGATGACGAGATGACCAAGTCCG	113
Db	129	AGTCGGCCAAAGAGGTCGAGACCAAGCACCATCGCTGCCATCCG	173

```

RESULT 36
US-08-105-168B-6/c
; Sequence 6, Application US/08105168B
; Patent No. 5589585
; GENERAL INFORMATION:
; APPLICANT: MABILAT et al.
; TITLE OF INVENTION: DNA FRAGMENTS OF MYCOBACTERIA, AMPLIFICATION
; TITLE OF INVENTION: PRIMERS, HYBRIDIZATION PROBES, REAGENTS AND METHOD FOR THE DETE
; TITLE OF INVENTION: MYCOBACTERIA
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Oliff & Berridge
; STREET: 700 South Washington Street, Suite 300
; CITY: Alexandria,
; STATE: Virginia
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" DS/HD
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS DOS 3.1
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; FILING DATE: August 12, 1993
; APPLICATION NUMBER: US/08/105,168B
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR9210094
; FILING DATE: August 8, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: William P. Berridge
; REGISTRATION NUMBER: 30,024
; REFERENCE/DOCKET NUMBER: WPB 28835
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6400
; TELEFAX: (703) 836-2787
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 200 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single-stranded

```

TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL:
ANTI-SENSE:
ORIGINAL SOURCE:
ORGANISM: Mycobacterium intracellulare
STRAIN:
INDIVIDUAL ISOLATE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
FEATURE:
NAME/KEY:
LOCATION: 518-717
IDENTIFICATION METHOD:
OTHER INFORMATION:
US-08-105-168B-6

Query Match 14.7%; Score 22.6; DB 1; Length 200;
Best Local Similarity 57.1%; Pred. No. 4.5e+03;
Matches 60; Conservative 0; Mismatches 44; Indels 1; Gaps 1;

QY 42 CGAGCTGTCATCTCGCTCATCTGAGATCGGCGCCGCACTCGACGATGAGCGAGA 101
DB 173 CGGTGGCAGCATCTGTCCTTGTCTCGACCTCCTTGCCGACTGAGCAGGCTCTCG 114
QY 102 TGACCAGCTCCGCGCCGCACTCGACGATGAGCGAGATGACCGAGC 146
DB 113 TGACCTTCT-CGACGCGCTTCTCGATGCCGCTTGAGACCGAGC 70

RESULT 37

US-08-698-948-6
Sequence 6, Application US/08698948
Patent No. 5849901

GENERAL INFORMATION:

APPLICANT: MABILAT et al.

TITLE OF INVENTION: DNA FRAGMENTS OF MYCOBACTERIA, AMPLIFICATION

TITLE OF INVENTION: PRIMERS, HYBRIDIZATION PROBES, REAGENTS AND METHOD FOR THE DET

TITLE OF INVENTION: MYCOBACTERIA

NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:

ADDRESSEE: Oliff & Berridge
STREET: 700 South Washington Street, Suite 300
CITY: Alexandria,
STATE: Virginia

ZIP: 22314

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" DS/HD

COMPUTER: IBM compatible
OPERATING SYSTEM: MS DOS 3.1

SOFTWARE: Wordperfect

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/698,948

FILING DATE: August 16, 1996

CLASSIFICATION: 536

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/105,168

FILING DATE: August 12, 1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR9210094

FILING DATE: August 8, 1992

ATTORNEY/AGENT INFORMATION:
NAME: William P. Berridge

REGISTRATION NUMBER: 30,024

REFERENCE/DOCKET NUMBER: WPB 28835A

TELEPHONE: (703) 836-6400

TELEFAX: (703) 836-2787

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:
LENGTH: 200 base pairs
TYPE: nucleic acid

STRANDEDNESS: single-stranded
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL:
ANTI-SENSE:
ORIGINAL SOURCE:
ORGANISM: Mycobacterium intracellulare
STRAIN:
INDIVIDUAL ISOLATE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
FEATURE:
NAME/KEY:
LOCATION: 518-717
IDENTIFICATION METHOD:
OTHER INFORMATION:
US-08-698-948-6

Query Match 14.7%; Score 22.6; DB 2; Length 200;
Best Local Similarity 57.1%; Pred. No. 4.5e+03;
Matches 60; Conservative 0; Mismatches 44; Indels 1; Gaps 1;

QY 9 GCTGTCATCTCGCTCATCTGAGTCGCGCGCCGAGCTGTCTCTGCTCATCTCG 68
DB 70 GCTGGTCTCAAGCGCGGCACTCGAGAGGCCGTC-GAGAAGTCAACCGAGACCTGCTCA 128
QY 69 AGTCGGGCGCCCGCACTCGACGATGAGCGAGATGACCAAGCTCCG 113
DB 129 AGTCGGCAAGAGAGTTCGAGACCAAGACCAAGATCGCTGCCACCG 173

RESULT 38

US-08-698-948-6/c
Sequence 6, Application US/08698948
Patent No. 5849901

GENERAL INFORMATION:

APPLICANT: MABILAT et al.

TITLE OF INVENTION: DNA FRAGMENTS OF MYCOBACTERIA, AMPLIFICATION

TITLE OF INVENTION: PRIMERS, HYBRIDIZATION PROBES, REAGENTS AND METHOD FOR THE DETI

TITLE OF INVENTION: MYCOBACTERIA

NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:

ADDRESSEE: Oliff & Berridge
STREET: 700 South Washington Street, Suite 300
CITY: Alexandria,
STATE: Virginia

ZIP: 22314

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" DS/HD

COMPUTER: IBM compatible
OPERATING SYSTEM: MS DOS 3.1

SOFTWARE: Wordperfect

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/698,948

FILING DATE: August 16, 1996

CLASSIFICATION: 536

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/105,168

FILING DATE: August 12, 1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR9210094

FILING DATE: August 8, 1992

ATTORNEY/AGENT INFORMATION:
NAME: William P. Berridge

REGISTRATION NUMBER: 30,024

REFERENCE/DOCKET NUMBER: WPB 28835A

TELEPHONE: (703) 836-6400

TELEFAX: (703) 836-2787

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:
LENGTH: 200 base pairs

```
; TYPE: nucleic acid
; STRANDEDNESS: single-stranded
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL:
; ANTI-SENSE:
; ORIGINAL SOURCE:
; ORGANISM: Mycobacterium intracellulare
; STRAIN:
; INDIVIDUAL ISOLATE:
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT:
; MAP POSITION:
; FEATURE:
; NAME/KEY:
; LOCATION: 518-717
; IDENTIFICATION METHOD:
; OTHER INFORMATION:
; US-08-698-948-6
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Query Match 14.7%; Score 22.6; DB 2; Length 200;
Best Local Similarity 57.1%; Pred. No. 4.5e+03;
Matches 60; Conservative 0; Mismatches 44; Indels 1; Gaps 1;
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OY 42 CGAGCTGTCATCTCGCTCATCTCGAGTCGGCGCCCGCACTCGACGATGAGCGAGA 101
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 173 CGGTGGAGCGATCTGTCCTTGTCTCGACCTCTTGCGCACTTGAGCAGGGTCTCGG 114

OY 102 TGACCAGCTCCGCGCCCGCACTCGACGATGAGCGAGATGACCAGC 146
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 113 TGACCTTCT-CGACGCGCTTCTCGATGCCGCGCTTGAGACCCAGC 70
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RESULT 39

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US-09-902-540-8045
; Sequence 8045, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 8045
; LENGTH: 174
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
; US-09-902-540-8045
```

```
Query Match 14.5%; Score 22.4; DB 4; Length 174;
Best Local Similarity 59.4%; Pred. No. 5e+03;
Matches 38; Conservative 0; Mismatches 26; Indels 0; Gaps 0;
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OY 40 GCCGAGCTGTCATCTCGCTCATCTCGAGTCGGCGCCCGCACTCGACGATGAGCGA 99
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 99 GCCGCGCGCGCGCGCTCGTATTCGGCGAGCTGCAAGCGCGCTACGAGAGCGCGTGT 158

OY 100 GATG 103
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Db 159 GAAG 162
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RESULT 40
US-09-902-540-8045/C
; Sequence 8045, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
```

```
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 8045
; LENGTH: 174
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
; US-09-902-540-8045
```

```
Query Match 14.5%; Score 22.4; DB 4; Length 174;
Best Local Similarity 59.4%; Pred. No. 5e+03;
Matches 38; Conservative 0; Mismatches 26; Indels 0; Gaps 0;
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OY 52 CATCTGCTCATCTGTCAGTCGGCGCCCGCACTCGACGATGAGCGAGATGACCAGCTC 111
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 162 CTTACACAGCGCTTCTCTGTAAGCGGCGCTGACGTCGCCGAATACCGAGCGCGCGCG 103

OY 112 CGGC 115
    |||
Db 102 CGGC 99
```

RESULT 41

```
US-09-902-540-7303
; Sequence 7303, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 7303
; LENGTH: 102
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
; US-09-902-540-7303
```

```
Query Match 14.3%; Score 22; DB 4; Length 102;
Best Local Similarity 57.1%; Pred. No. 6.1e+03;
Matches 40; Conservative 0; Mismatches 30; Indels 0; Gaps 0;
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OY 1 CGCGGAGCTGTGTCATCTCGCTCATCTCGAGTCGGCGCCCGGAGCTGTCATCTCGCT 60
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 6 CTGGCGACGCTGTCTCTGTAAGCGGCGCTGAGGCGCGCGCGCGCGCGGATGCGGCC 65

OY 61 CATGTCGAG 70
    ||| ||| |||
Db 66 CGACGTGGCG 75
```

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RESULT 42
US-09-902-540-7303/C
; Sequence 7303, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
```



```

; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 7303
; LENGTH: 102
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
; US-09-902-540-7303

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Query Match          14.3%; Score 22; DB 4; Length 102;
Best Local Similarity 57.1%; Pred. No. 6.1e+03;
Matches 40; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

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QY 85 CTCGACGATGACGACGATGACGACGCTCCGCGCCGACCTCGACGATGAGCGAGATGACCA 144
    |||||
Db 75 CGCCACGTCGCGCGCCCATCACCGCGCGCGCGCCCGCCGAGTACGAGGACAG 16
QY 145 GCTCCGCGCCG 154
    |||||
Db 15 GCTGCGCCAG 6

```

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RESULT 43
US-09-313-294A-6924
; Sequence 6924, Application US/09313294A
; Patent No. 6476212
; GENERAL INFORMATION:
; APPLICANT: Lalgudi, Raghunath V.
; APPLICANT: Ito, Laura Y.
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
; FILE REFERENCE: PL-0017 US
; CURRENT APPLICATION NUMBER: US/09/313,294A
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 7600
; SOFTWARE: PERL Program
; SEQ ID NO 6924
; LENGTH: 164
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6476212 700380851H1
; NAME/KEY: unsure
; LOCATION: 22, 60, 64, 76, 83, 85
; OTHER INFORMATION: a, t, c, g, or other
; US-09-313-294A-6924

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Query Match          14.3%; Score 22; DB 4; Length 164;
Best Local Similarity 48.6%; Pred. No. 6.2e+03;
Matches 52; Conservative 0; Mismatches 55; Indels 0; Gaps 0;
QY 3 GCCGAGCTGTCATCTGCTCATCTGTCAGTCGCGCGCGCGAGCTGTCATCTGCTCA 62
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Db 58 GCNGGTNGTGTCTCCCTCTCNCNCCGCGCGCGCGCGCGAGCGGGGAGTCCCA 117
QY 63 TCGTCAGTCGCGCGCGCGCGCGAGTGCAGGATGAGGATGACCAAGC 109
    |||||
Db 118 AACCTAGTGGAGTTGAGACTAGAGGAGGCGCGAGATCCGCGC 164

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RESULT 44
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; Sequence 6924, Application US/09313294A
; Patent No. 6476212
; GENERAL INFORMATION:
; APPLICANT: Lalgudi, Raghunath V.
; APPLICANT: Ito, Laura Y.

```

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; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
; FILE REFERENCE: PL-0017 US
; CURRENT APPLICATION NUMBER: US/09/313,294A
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 7600
; SOFTWARE: PERL Program
; SEQ ID NO 6924
; LENGTH: 164
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6476212 700380851H1
; NAME/KEY: unsure
; LOCATION: 22, 60, 64, 76, 83, 85
; OTHER INFORMATION: a, t, c, g, or other
; US-09-313-294A-6924

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Query Match          14.3%; Score 22; DB 4; Length 164;
Best Local Similarity 48.6%; Pred. No. 6.2e+03;
Matches 52; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

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QY 46 GCTGTCATCTGCTCATCTGTCAGTCGCGCGCGCGCGACTCGACGATGAGCGAGATGAC 105
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QY 106 CAGCTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC 152
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RESULT 45
US-09-902-540-8725
; Sequence 8725, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 8725
; LENGTH: 180
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
; US-09-902-540-8725

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Best Local Similarity 49.2%; Pred. No. 6.3e+03;
Matches 58; Conservative 0; Mismatches 60; Indels 0; Gaps 0;
QY 36 GCGCGCGCGAGCTGTCATCTGCTCATCTGTCAGTCGCGCGCGCGCGCGCGCGCGCGCGCGC 95
    |||||
Db 11 GCCGATGACGCCGACGAGTGGACATCTCCATGTGATACGGCGAGCGCGTGACGC 70
QY 96 GCGAGATGACCACTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC 153
    |||||
Db 71 TGACGATGCCAGCTTCTGTCTCAACAAGGTGTTCCGCTGGGTGACACGCGCGCGC 128

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Search completed: April 9, 2005, 02:34:14
Job time: 133 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 8, 2005, 23:27:07 ; Search time 424 Seconds
(without alignments)
2150.095 Million cell updates/sec

Title: US-09-887-194A-13

Perfect score: 154

Sequence: 1 cggcgcgagctggtcatctc.....gagatgaccagctccgcg 154

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 4887668

Minimum DB seq length: 0

Maximum DB seq length: 200

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

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- 1: geneseqn1980s:*
- 2: geneseqn1990s:*
- 3: geneseqn2000s:*
- 4: geneseqn2001as:*
- 5: geneseqn2001bs:*
- 6: geneseqn2002as:*
- 7: geneseqn2002bs:*
- 8: geneseqn2003as:*
- 9: geneseqn2003bs:*
- 10: geneseqn2003cs:*
- 11: geneseqn2003ds:*
- 12: geneseqn2004as:*
- 13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	154	100.0	154	6	AAD29231	Aad29231 Plasmids
2	154	100.0	154	6	AAD29231	Aad29231 Plasmids
3	154	100.0	154	6	AAD32908	Aad32908 Plasmid p
4	154	100.0	154	6	AAD32908	Aad32908 Plasmid p
5	154	100.0	154	12	ADQ07968	Adq07968 Seed spec
6	154	100.0	154	12	ADQ07968	Adq07968 Seed spec
7	81	52.6	81	6	ABK10711	Abk10711 Artificia
8	81	52.6	81	6	ABK10711	Abk10711 Artificia
9	80	51.9	80	6	AAD29230	Aad29230 Plasmids
10	80	51.9	80	6	AAD29230	Aad29230 Plasmids
11	80	51.9	80	6	AAD32907	Aad32907 Plasmids
12	80	51.9	80	6	AAD32907	Aad32907 Plasmids
13	80	51.9	92	6	ABK10712	Abk10712 Artificia
14	80	51.9	92	6	ABK10712	Abk10712 Artificia
15	80	51.9	92	6	AAD29232	Aad29232 ELVISLIVE
16	80	51.9	92	6	AAD29232	Aad29232 ELVISLIVE
17	44	28.6	44	6	ABK10710	Abk10710 Artificia
18	44	28.6	44	6	ABK10710	Abk10710 Artificia
19	29.4	19.1	194	4	AAC89216	Aac89216 Human bra
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21	28	18.2	197	10	ABX88193	Abx88193 Corn ear-
22	28	18.2	197	10	ABX88193	Abx88193 Corn ear-
23	26.6	17.3	156	6	AA144709	AA144709 Human glu
24	26.6	17.3	156	6	AA144709	AA144709 Human glu
25	26.6	17.3	190	6	AA144706	AA144706 Human glu
26	26.6	17.3	190	6	AA144706	AA144706 Human glu
27	26.6	17.3	195	3	AAC09904	Aac09904 Human sec
28	26.6	17.3	195	3	AAC09904	Aac09904 Human sec
29	26	16.9	170	4	AA117387	AA117387 Human bre
30	26	16.9	170	4	AA117387	AA117387 Human bre
31	26	16.9	189	4	AA109498	AA109498 Human bre
32	26	16.9	189	4	AA109498	AA109498 Human bre
33	25.6	16.6	183	2	AA149353	AA149353 N. fische
34	25.6	16.6	183	2	AA149353	AA149353 N. fische
35	25	16.2	123	3	AAA94339	AAA94339 123-mer D
36	25	16.2	123	3	AAA94339	AAA94339 123-mer D
37	24.8	16.1	108	12	ACH88658	Ach88658 Human gen
38	24.8	16.1	108	12	ACH88658	Ach88658 Human gen
39	24.8	16.1	130	10	ACD96616	AcD96616 Human col
40	24.8	16.1	130	10	ACD96616	AcD96616 Human col
41	24.8	16.1	181	3	AA12537	AA12537 Human sec
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43	24.4	15.8	164	7	ADS69652	Ads69652 Corn seed
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45	24.4	15.8	185	4	AA127481	AA127481 Probe #17
46	24.4	15.8	185	4	AA127481	AA127481 Probe #17
47	24.4	15.8	185	4	ABA75795	AbA75795 Human foe
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49	24.4	15.8	185	4	AA156451	AA156451 Probe #25
50	24.4	15.8	185	4	AA156451	AA156451 Probe #25
51	24.4	15.8	185	4	ABA40366	ABA40366 Probe #18
52	24.4	15.8	185	4	ABA40366	ABA40366 Probe #18
53	24.4	15.8	185	4	AAK50468	AAk50468 Human bon
54	24.4	15.8	185	4	AAK50468	AAk50468 Human bon
55	24.4	15.8	185	4	AAK24480	AAk24480 Human bra
56	24.4	15.8	185	4	ABS50091	AbS50091 Human liv
57	24.4	15.8	185	4	ABS50091	AbS50091 Human liv
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59	24.4	15.8	185	6	ABS23940	AbS23940 Human gen
60	24.4	15.8	185	6	AA193196	AA193196 Synthetic
61	24.2	15.7	175	2	AA193196	AA193196 Synthetic
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67	24.2	15.7	175	12	ADQ28293	AdQ28293 Abbot-mo
68	24.2	15.7	175	12	ADQ28293	AdQ28293 Abbot-mo
69	23.6	15.3	71	3	AA11674	AAc11674 Human sec
70	23.6	15.3	71	3	AA11674	AAc11674 Human sec
71	23.6	15.3	178	10	ACD93885	AcD93885 Human col
72	23.6	15.3	178	10	ACD93885	AcD93885 Human col
73	23.4	15.2	121	12	ADL80636	AdL80636 Human rec
74	23.4	15.2	121	12	ADL80636	AdL80636 Human rec
75	23.2	15.1	132	9	ADA49202	Ada49202 Maize gen
76	23.2	15.1	132	9	ADA49202	Ada49202 Maize gen
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78	23.2	15.1	192	6	ABK44945	AbK44945 CDNA enco
79	23	14.9	74	4	AA158508	AA158508 Nucleotid
80	23	14.9	74	4	AA158508	AA158508 Nucleotid
81	23	14.9	74	10	ADF17445	Adf17445 IL-1 rece
82	23	14.9	74	10	ADF17445	Adf17445 IL-1 rece
83	23	14.9	74	10	ADF53650	Adf53650 Phosphata
84	23	14.9	74	10	ADF53650	Adf53650 Phosphata
85	23	14.9	74	10	ADF44538	Adf44538 Mouse kin
86	23	14.9	74	10	ADF44538	Adf44538 Mouse kin
87	23	14.9	74	10	ADF74728	Adf74728 Synthetic
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91	23	14.9	74	12	ADF50664	Adf50664 Sequencin
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c	94	23	14.9	74	12	ADG31227	Adg31227 Novel mou
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c	98	23	14.9	176	6	ABK16750	Abk16750 Human CDN
c	99	23	14.9	192	6	ABQ91010	Abq91010 M. capsul
c	100	23	14.9	192	6	ABQ91010	Abq91010 M. capsul

ALIGNMENTS

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RESULT 1
AAD29231
ID   AAD29231 standard; DNA; 154 BP.
XX
XX   AAD29231;
XX
XX   07-MAY-2002 (first entry)
XX
XX   Plasmids pKS133 2X ELVISLIVES complementary repeat DNA.
XX
XX   Recombinant construct; gene expression; plasmid pKS133; ds.
XX
XX   Unidentified.
XX
XX   Key      Location/Qualifiers
XX   CDS      7..36
XX            /*tag= a
XX            /product= "ELVISLIVES protein"
XX
XX   CDS      44..74
XX            /*tag= b
XX            /product= "ELVISLIVES protein"
XX
XX   CDS      /*tag= c
XX            /product= "ELVISLIVES protein"
XX            complement(119..148)
XX            /*tag= d
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XX
XX   WO200200904-A2.
XX
XX   03-JAN-2002.
XX
XX   22-JUN-2001; 2001WO-US019962.
XX
XX   23-JUN-2000; 2000US-0213961P.
XX
XX   (DUPO ) DU PONT DE NEMOURS & CO E I.
XX   (PION-) PIONEER HI-BRED INT INC.
XX
XX   Glassman KF, Gordon-Kamm WJ, Kinney AJ, Lowe K, Stecca KL,
XX   Nichols SE;
XX
XX   WPI; 2002-139927/18.
XX   P-PSDB; AAE18333.
XX
XX   New recombinant construct having a promoter operably linked to a DNA
XX   sequence which when expressed produces an RNA having homology to a target
XX   mRNA and its reverse complement unrelated to endogenous DNA, for reducing
XX   gene expression.
XX
XX   Claim 45; Page 37; 77pp; English.
XX
XX   The present invention relates to a new recombinant construct. The
XX   construct comprises a promoter operably linked to a DNA sequence which
XX   when expressed by a host produces an RNA having homology to at least one
XX   target mRNA expressed by the host and complementary RNA regions. The
XX   recombinant construct is useful for reducing the expression of a target
XX   mRNA or any similar endogenous mRNA. The RNAs expressed from the
XX   recombinant constructs are also used in reducing expression of a target
XX   mRNA or any similar endogenous mRNA. The sequences and their reverse
XX   complements can be used to reduce the expression of any endogenous
```

CC genomic sequence that shares substantial similarity to nucleic acid
CC fragment which is in proximity to the DNA or RNA sequence derived from
CC it. The present sequence is 2X ELVISLIVES complementary repeat region DNA
CC found in plasmid pKS133 used in the exemplification of the invention
XX
SQ Sequence 154 BP; 24 A; 53 C; 53 G; 24 T; 0 U; 0 Other;

Query Match 100.0%; Score 154; DB 6; Length 154;
Best Local Similarity 100.0%; Pred. No. 2.7e-28;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1 CGGCGGAGCTGTCATCTCGCTCATCGTCGAGTCGGCGCGGAGCTGTCATCTCGCT 60
    |||
Db 1 CGGCCGAGCTGTCATCTCGCTCATCGTCGAGTCGGCGCGGAGCTGTCATCTCGCT 60
OY 61 CATCGTCAGTCGGCGCGCGCGGAGCTCGACGATGACCGAGATGACCACTCCGCCGCCG 120
    |||
Db 61 CATCGTCAGTCGGCGCGCGCGGAGCTCGACGATGACCGAGATGACCACTCCGCCGCCG 120
OY 121 ACTCGACGATGACCGAGATGACCACTCCGCCGCCG 154
    |||
Db 121 ACTCGACGATGACCGAGATGACCACTCCGCCGCCG 154
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RESULT 2
AAD29231/c
ID   AAD29231 standard; DNA; 154 BP.
XX
XX   AAD29231;
XX
XX   07-MAY-2002 (first entry)
XX
XX   Plasmids pKS133 2X ELVISLIVES complementary repeat DNA.
XX
XX   Recombinant construct; gene expression; plasmid pKS133; ds.
XX
XX   Unidentified.
XX
XX   Key      Location/Qualifiers
XX   CDS      7..36
XX            /*tag= a
XX            /product= "ELVISLIVES protein"
XX
XX   CDS      44..74
XX            /*tag= b
XX            /product= "ELVISLIVES protein"
XX            complement(82..111)
XX
XX   CDS      /*tag= c
XX            /product= "ELVISLIVES protein"
XX            complement(119..148)
XX            /*tag= d
XX            /product= "ELVISLIVES protein"
XX
XX   WO200200904-A2.
XX
XX   03-JAN-2002.
XX
XX   22-JUN-2001; 2001WO-US019962.
XX
XX   23-JUN-2000; 2000US-0213961P.
XX
XX   (DUPO ) DU PONT DE NEMOURS & CO E I.
XX   (PION-) PIONEER HI-BRED INT INC.
XX
XX   Glassman KF, Gordon-Kamm WJ, Kinney AJ, Lowe K, Stecca KL,
XX   Nichols SE;
XX
XX   WPI; 2002-139927/18.
XX   P-PSDB; AAE18333.
XX
XX   New recombinant construct having a promoter operably linked to a DNA
XX   sequence which when expressed produces an RNA having homology to a target
XX   mRNA and its reverse complement unrelated to endogenous DNA, for reducing
XX   gene expression.
```

```
XX PS Claim 45; Page 37; 77pp; English.
XX CC The present invention relates to a new recombinant construct. The
CC CC construct comprises a promoter operably linked to a DNA sequence which
CC CC when expressed by a host produces an RNA having homology to at least one
CC CC target mRNA expressed by the host and complementary RNA regions. The
CC CC recombinant construct is useful for reducing the expression of a target
CC CC mRNA or any similar endogenous mRNA. The RNAs expressed from the
CC CC recombinant constructs are also used in reducing expression of a target
CC CC mRNA or any similar endogenous mRNA. The sequences and their reverse
CC CC complements can be used to reduce the expression of any endogenous
CC CC genomic sequence that shares substantial similarity to nucleic acid
CC CC fragment which is in proximity to the DNA or RNA sequence derived from
CC CC it. The present sequence is 2X ELVISLIVES complementary repeat region DNA
CC CC found in plasmid pKS133 used in the exemplification of the invention
XX SQ Sequence 154 BP; 24 A; 53 C; 53 G; 24 T; 0 U; 0 Other;

Query Match          100.0%; Score 154; DB 6; Length 154;
Best Local Similarity 100.0%; Pred. No. 2.7e-28;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CGGCCGAGCTGTGTCATCTCGCTCATCTGTCGAGTCGGCGCGGAGCTGTGTCATCTCGCT 60
DB 154 CGGCCGAGCTGTGTCATCTCGCTCATCTGTCGAGTCGGCGCGGAGCTGTGTCATCTCGCT 95

OY 61 CATCGTCGAGTCGGCGCGCGCGGAGCTCGACGATGAGCGAGATGACCACTCCGGCCGCG 120
DB 94 CATCGTCGAGTCGGCGCGCGCGGAGCTCGACGATGAGCGAGATGACCACTCCGGCCGCG 35

OY 121 ACTCGACGATGAGCGAGATGACCACTCCGGCCG 154
DB 34 ACTCGACGATGAGCGAGATGACCACTCCGGCCG 1

RESULT 3
AAD32908
ID AAD32908 standard; DNA; 154 BP.
XX AC AAD32908;
XX DT 01-JUL-2002 (first entry)
XX DE Plasmid pKS133 2X ELVISLIVES complementary repeat DNA.
XX KW Rice; diverged delta-9 fatty acid desaturase; enzyme; cellular lipid;
KW oil; transgenic plant; gene mapping; immunisation; plasmid pKS133; gene;
XX ds.
XX OS Unidentified.
XX FH Key Location/Qualifiers
FH CDS 7..36
FT /*tag= a
FT /*product= "ELVISLIVES protein"
FT CDS 44..74
FT /*tag= b
FT /*product= "ELVISLIVES protein"
FT CDS complement(82..111)
FT /*tag= c
FT /*product= "ELVISLIVES protein"
FT CDS complement(119..148)
FT /*tag= d
FT /*product= "ELVISLIVES protein"
XX OS
XX PN WO200216565-A2.
XX PD 28-FEB-2002.
XX PF 22-AUG-2001; 2001WO-US026246.
XX PR 22-AUG-2000; 2000US-0226996P.
```

```
XX PA (DUPO ) DU PONT DE NEMOURS & CO E I.
XX PI Booth JR, Cahoon RE, Hitz WD, Kinney AJ, Yadav NS;
XX DR WPI; 2002-269353/31.
XX DR P-PSDB; AAB20554.
XX PT New delta-9 fatty acid desaturase polypeptides and polynucleotides,
PT useful in creating transgenic plants having altered levels of mono-, poly
PT - and unsaturated fatty acids and in increasing the unsaturation levels
PT in cellular lipids.
XX PS Example 9; Page 43; 77pp; English.
XX CC The present invention relates to diverged delta-9 fatty acid desaturase
CC CC proteins and polynucleotides encoding such proteins. The nucleic acid
CC CC sequences may be used to increase the level of unsaturation in cellular
CC CC lipids, including oil, in tissues when the enzyme is absent or rate-
CC CC limiting, to isolate cDNAs and genes encoding homologous proteins from
CC CC the same or other plant species and to create transgenic plants in which
CC CC the polypeptides are present at higher or lower levels than normal or in
CC CC cell types or developmental stages in which they are not normally found,
CC CC thus altering the level of mono-, poly- and unsaturated fatty acids in
CC CC those cells. They are useful as probes for genetic and physical gene
CC CC mapping and as markers, e.g. restriction fragment length polymorphism
CC CC (RFLP) markers. The peptides can be used to immunise animals to produce
CC CC antibodies specific for the peptides and proteins. The present sequence
CC CC is 1X ELVISLIVES complementary repeat region DNA found in plasmid pKS133
CC CC This sequence is used in the exemplification of the invention for the
CC CC suppression of Fad2 in soybean
XX SQ Sequence 154 BP; 24 A; 53 C; 53 G; 24 T; 0 U; 0 Other;

Query Match          100.0%; Score 154; DB 6; Length 154;
Best Local Similarity 100.0%; Pred. No. 2.7e-28;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CGGCCGAGCTGTGTCATCTCGCTCATCTGTCGAGTCGGCGCGGAGCTGTGTCATCTCGCT 60
DB 1 CGGCCGAGCTGTGTCATCTCGCTCATCTGTCGAGTCGGCGCGGAGCTGTGTCATCTCGCT 60

OY 61 CATCGTCGAGTCGGCGCGCGCGGAGCTCGACGATGAGCGAGATGACCACTCCGGCCGCG 120
DB 61 CATCGTCGAGTCGGCGCGCGCGGAGCTCGACGATGAGCGAGATGACCACTCCGGCCGCG 120

OY 121 ACTCGACGATGAGCGAGATGACCACTCCGGCCG 154
DB 121 ACTCGACGATGAGCGAGATGACCACTCCGGCCG 154

RESULT 4
AAD32908/c
ID AAD32908 standard; DNA; 154 BP.
XX AC AAD32908;
XX DT 01-JUL-2002 (first entry)
XX DE Plasmid pKS133 2X ELVISLIVES complementary repeat DNA.
XX KW Rice; diverged delta-9 fatty acid desaturase; enzyme; cellular lipid;
KW oil; transgenic plant; gene mapping; immunisation; plasmid pKS133; gene;
XX ds.
XX OS Unidentified.
XX FH Key Location/Qualifiers
FH CDS 7..36
FT /*tag= a
FT /*product= "ELVISLIVES protein"
FT CDS 44..74
FT /*tag= b
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FT      CDS      /product= "ELVISLIVES protein"
FT      complement(82. .111)
FT      /tag= c
FT      /product= "ELVISLIVES protein"
FT      complement(119. .148)
FT      /tag= d
FT      /product= "ELVISLIVES protein"
XX      WO200216565-A2.
XX      PD      28-FEB-2002.
XX      PF      22-AUG-2001; 2001WO-US026246.
XX      PR      22-AUG-2000; 2000US-0226996P.
XX      PA      (DUPO ) DU PONT DE NEMOURS & CO E I.
XX      PI      Booth JR, Cahoon RE, Hiltz WD, Kinney AJ, Yadav NS;
XX      XX      WPI; 2002-269353/31.
XX      DR      P-PSDB; AAE20554.
XX      PT      New delta-9 fatty acid desaturase polypeptides and polynucleotides,
XX      PT      useful in creating transgenic plants having altered levels of mono-, poly
XX      PT      - and unsaturated fatty acids and in increasing the unsaturation levels
XX      PT      in cellular lipids.
XX      PS      Example 9; Page 43; 77pp; English.
XX      CC      The present invention relates to diverged delta-9 fatty acid desaturase
XX      CC      proteins and polynucleotides encoding such proteins. The nucleic acid
XX      CC      sequences may be used to increase the level of unsaturation in cellular
XX      CC      lipids, including oil, in tissues when the enzyme is absent or rate-
XX      CC      limiting, to isolate cDNAs and genes encoding homologous proteins from
XX      CC      the same or other plant species and to create transgenic plants in which
XX      CC      the polypeptides are present at higher or lower levels than normal or in
XX      CC      cell types or developmental stages in which they are not normally found,
XX      CC      thus altering the level of mono-, poly- and unsaturated fatty acids in
XX      CC      those cells. They are useful as probes for genetic and physical gene
XX      CC      mapping and as markers, e.g. restriction fragment length polymorphism
XX      CC      (RFLP) markers. The peptides can be used to immunise animals to produce
XX      CC      antibodies specific for the peptides and proteins. The present sequence
XX      CC      is 1X ELVISLIVES complementary repeat region DNA found in plasmid PKS133
XX      CC      This sequence is used in the exemplification of the invention for the
XX      CC      suppression of Fad2 in soybean
XX      SQ      Sequence 154 BP; 24 A; 53 C; 53 G; 24 T; 0 U; 0 Other;
XX
XX      Query Match      100.0%; Score 154; DB 6; Length 154;
XX      Best Local Similarity 100.0%; Pred. No. 2.7e-28;
XX      Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY      1 CGGCCGGAGCTGTCATCTCGCTCATCTCGAGTCGGCGCCGGAGCTGGTCAATCTCGCT 60
QY      154 CGGCCGGAGCTGTCATCTCGCTCATCTCGAGTCGGCGCCGGAGCTGGTCAATCTCGCT 95
Db
QY      61 CATCGTCGAGTCGGCGCCGGAGCTCGACGATGAGCGAGATGACCAAGCTCCGGCCGG 120
Db      94 CATCGTCGAGTCGGCGCCGGAGCTCGACGATGAGCGAGATGACCAAGCTCCGGCCGG 35
QY      121 ACTCGACGATGAGCGAGATGACCAAGCTCCGGCCGG 154
Db      34 ACTCGACGATGAGCGAGATGACCAAGCTCCGGCCGG 1
XX
RESULT 5
ADQ07968
ID      ADQ07968 standard; DNA; 154 BP.
XX
AC      ADQ07968;
XX
DT      23-SEP-2004 (first entry)
```

```
XX      DE      Seed specific gene silencing vector pKS151, stem loop region.
XX      XX      PKS151; seed specific promoter; gene silencing; chalcone reductase;
XX      KW      transgenic; liquiritigenin-derived isoflavone; isoflavonoid;
XX      KW      food product; snack food product; baked good product; fried food product;
XX      KW      health food product; infant formula; beverage; nutritional supplement;
XX      KW      dairy product; pet food product; animal feed; ss.
XX      OS      Synthetic.
XX      FH      Key      Location/Qualifiers
XX      FT      stem_loop      1. .154
XX      FT      /tag= a
XX      PN      US2004128714-A1.
XX      PD      01-JUL-2004.
XX      PF      11-DEC-2003; 2003US-00734947.
XX      PR      13-DEC-2002; 2002US-0433433P.
XX      PA      (MCGO/) MCGONIGLE B.
XX      PI      Mgonigle B;
XX      DR      WPI; 2004-533136/51.
XX      PT      Decreasing ratio of liquiritigenin-derived isoflavones relative to total
XX      PT      isoflavones in a plant comprises transforming plant cell with nucleic
XX      PT      acid sequence showing homology to sequence encoding chalcone reductase
XX      PT      (deoxychalcone synthase).
XX      PS      Example 7; SEQ ID NO 7; 25pp; English.
XX      CC      The invention relates to decreasing the ratio of liquiritigenin-derived
XX      CC      isoflavones relative to the total isoflavones in an isoflavonoid-
XX      CC      producing plant comprising transforming a plant cell with a recombinant
XX      CC      construct comprising a promoter operably linked to a nucleic acid
XX      CC      sequence of at least 200 nucleotides having at least 75% sequence
XX      CC      identity to ADQ07965 (a soybean chalcone reductase cDNA). Also included
XX      CC      are an isoflavonoid-producing plant made by the method above, seeds or
XX      CC      plant parts of the plant, an isoflavonoid-containing isoflavones relative to
XX      CC      the total isoflavone levels obtained from the seeds or plant parts, a
XX      CC      food (or a nutritional supplement, a food bar, or a beverage) which has
XX      CC      incorporated an isoflavonoid-containing product, and a method of
XX      CC      producing an isoflavonoid-containing product having a reduced ratio of
XX      CC      liquiritigenin-derived isoflavones relative to the total isoflavone
XX      CC      levels. The recombinant construct comprises a stem-loop structure. The
XX      CC      nucleic acid sequence forms a loop in the stem-loop structure and the
XX      CC      stem comprises a sequence of ADQ07968). The promoter is a seed-specific
XX      CC      promoter. The method is useful for decreasing the ratio of liquiritigenin
XX      CC      -derived isoflavones relative to the total isoflavones in an isoflavone-
XX      CC      producing plant. The methods and recombinant construct are useful in
XX      CC      producing an isoflavonoid-containing product which is incorporated in
XX      CC      cereal food product, snack food product, baked good product, fried food
XX      CC      product, health food product, infant formula, beverage, nutritional
XX      CC      supplement, dairy product, pet food product, or animal feed. The present
XX      CC      sequence is the single stranded version of the stem loop region from
XX      CC      plasmid PKS151.
XX      SQ      Sequence 154 BP; 24 A; 53 C; 53 G; 24 T; 0 U; 0 Other;
XX
XX      Query Match      100.0%; Score 154; DB 12; Length 154;
XX      Best Local Similarity 100.0%; Pred. No. 2.7e-28;
XX      Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY      1 CGGCCGGAGCTGTCATCTCGCTCATCTCGAGTCGGCGCCGGAGCTGGTCAATCTCGCT 60
Db      1 CGGCCGGAGCTGTCATCTCGCTCATCTCGAGTCGGCGCCGGAGCTGGTCAATCTCGCT 60
```

Qy 61 CATCGTCACTCGCGCCCGCACTCGACGATGAGCGAGATGACCAGCTCCGCCGCCG 120
CC ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 61 CATCGTCACTCGCGCCCGCACTCGACGATGAGCGAGATGACCAGCTCCGCCGCCG 120
Qy 121 ACTCGACGATGAGCGAGATGACCACTCCGCCGCCG 154
CC ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 ACTCGACGATGAGCGAGATGACCACTCCGCCGCCG 154
RESULT 6
ADQ07968/C ADQ07968 standard; DNA; 154 BP.
XX ID
AC ADQ07968;
XX
DT 23-SEP-2004 (first entry)
XX
DE Seed specific gene silencing vector pKSI51, stem loop region.
XX
KM pKSI51; seed specific promoter; gene silencing; chalcone reductase;
KM transgenic; liquiritigenin-derived isoflavone; isoflavonoid;
KM food product; snack food product; baked good product; fried food product;
KM health food product; infant formula; beverage; nutritional supplement;
KM dairy product; pet food product; animal feed; sb.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT stem_loop 1..154
FT /*tag= a
XX
PN US2004128714-A1.
XX
PD 01-JUL-2004.
XX
PF 11-DEC-2003; 2003US-00734947.
XX
PR 13-DEC-2002; 2002US-0433433P.
XX
PA (MCGO/) MCGONIGLE B.
XX
PI Mcgonigle B;
XX
DR WPI; 2004-533136/51.
XX
PT Decreasing ratio of liquiritigenin-derived isoflavones relative to total
PT isoflavones in a plant comprises transforming plant cell with nucleic
PT acid sequence showing homology to sequence encoding chalcone reductase
PT (deoxychalcone synthase).
XX
PS Example 7; SEQ ID NO 7; 25pp; English.
XX
CC The invention relates to decreasing the ratio of liquiritigenin-derived
CC isoflavones relative to the total isoflavones in an isoflavonoid-
CC producing plant comprising transforming a plant cell with a recombinant
CC construct comprising a promoter operably linked to a nucleic acid
CC sequence of at least 200 nucleotides having at least 75% sequence
CC identity to ADQ07965 (a soybean chalcone reductase cDNA). Also included
CC are an isoflavonoid-producing plant made by the method above, seeds or
CC plant parts of the plant, an isoflavonoid-containing protein product
CC having a reduced ratio of liquiritigenin-derived isoflavones relative to
CC the total isoflavone levels obtained from the seeds or plant parts, a
CC food (or a nutritional supplement, a food bar, or a beverage) which has
CC incorporated the isoflavonoid-containing product, and a method of
CC producing an isoflavonoid-containing product having a reduced ratio of
CC liquiritigenin-derived isoflavones relative to the total isoflavone
CC levels. The recombinant construct comprises a stem-loop structure. The
CC nucleic acid sequence forms a loop in the stem-loop structure and the
CC stem comprises a sequence of ADQ07968). The promoter is a seed-specific
CC promoter. The method is useful for decreasing the ratio of liquiritigenin
CC -derived isoflavones relative to the total isoflavones in an isoflavone-
CC producing plant. The methods and recombinant construct are useful in
CC producing an isoflavonoid-containing product which is incorporated in

CC cereal food product, snack food product, baked good product, fried food
CC product, health food product, infant formula, beverage, nutritional
CC supplement, dairy product, pet food product, or animal feed. The present
CC sequence is the single stranded version of the stem loop region from
CC plasmid pKSI51.
XX
SQ Sequence 154 BP; 24 A; 53 C; 53 G; 24 T; 0 U; 0 Other;
Query Match 100.0%; Score 154; DB 12; Length 154;
Best: Local Similarity 100.0%; Pred. No. 2.7e-28;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CGCCCGAGCTGTGTCATCTGCTCATGTCGAGTCGCGCCCGAGAGCTGTCATCTCGCT 60
CC ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 154 CGCCCGAGCTGTGTCATCTGCTCATGTCGAGTCGCGCCCGAGAGCTGTCATCTCGCT 95
Qy 61 CATCGTCACTCGCGCCCGCACTCGACGATGAGCGAGATGACCAGCTCCGCCGCCG 120
CC ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 94 CATCGTCACTCGCGCCCGCACTCGACGATGAGCGAGATGACCAGCTCCGCCGCCG 35
Qy 121 ACTCGACGATGAGCGAGATGACCACTCCGCCGCCG 154
CC ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 34 ACTCGACGATGAGCGAGATGACCACTCCGCCGCCG 1
RESULT 7
ABK10711
ID ABK10711 standard; DNA; 81 BP.
XX
AC ABK10711;
XX
DT 05-JUN-2002 (first entry)
XX
DE Artificial DNA sequence #3.
XX
KM Plasmidic phosphoglucomutase; transgenic; plant; gene; ds.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT CDS 7..36
FT /*tag= a
FT /product= "ELVISLIVES peptide"
FT /partial
FT /note= "No start or stop codon shown"
FT CDS 44..73
FT /*tag= b
FT /product= "ELVISLIVES peptide"
FT /partial
FT /note= "No start or stop codon shown"
XX
PN EP1174510-A2.
XX
PD 23-JAN-2002.
XX
PF 17-JUL-2001; 2001EP-00306143.
XX
PR 17-JUL-2000; 2000US-0218712P.
XX
PA (DUPO) DU PONT DE NEMOURS & CO E I.
XX
PI Allen SM, Butler KH, Carlson TJ, Ilag LB;
XX
DR WPI; 2002-156692/21.
DR P-PSDB; AAU77109.
XX
PT Novel isolated polypeptides having phosphoglucomutase activity and
PT polynucleotides encoding the polypeptides, useful for producing
PT transgenic plants with altered plasmidic phosphoglucomutase protein
PT levels.
XX
PS Example 9; Page 19; 27pp; English.
XX

CC The invention relates to plastidic phosphoglucomutase polypeptides and
CC their related nucleic acids. The sequences are useful for producing a
CC transgenic plant, by transforming a plant cell with a polynucleotide of
CC the invention and regenerating a plant from the transformed plant cell.
CC Polynucleotide fragments are useful for suppressing the level of
CC expression of a gene encoding a polypeptide having plastidic
CC phosphoglucomutase activity. An isolated polynucleotide that affects the
CC level of expression of a plastidic phosphoglucomutase polypeptide in a
CC plant cell can be identified by introducing a DNA fragment comprising at
CC least 541 nucleotides, measuring the level of the polypeptide in the
CC plant cell containing the polynucleotide, and comparing the level of the
CC polypeptide in the plant cell containing the isolated polynucleotide with
CC the level of the polypeptide in a plant cell that does not contain the
CC isolated polynucleotide. A method for altering the level of expression of
CC a plastidic phosphoglucomutase protein in a host cell comprises
CC transforming a host cell with a chimeric gene and growing the transformed
CC cell under conditions that are suitable for expression of the chimeric
CC gene, where the expression of the gene results in production of altered
CC levels of plastidic phosphoglucomutase. This sequence represents an
CC artificial DNA used for plasmid construction, in the methods of the
CC invention

CC Sequence 81 BP; 8 A; 28 C; 29 G; 16 T; 0 U; 0 Other;

Query Match 52.6%; Score 81; DB 6; Length 81;
Best Local Similarity 100.0%; Pred. No. 1.3e-10;
Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CGGCCGAGCTGCTCATCTCGCTCATCGAGTCGCGCGCGGAGCTGTCTCATCTCGCT 60
|||
DB 1 CGGCCGAGCTGCTCATCTCGCTCATCGAGTCGCGCGCGGAGCTGTCTCATCTCGCT 60

OY 61 CATCGTCGAGTCGCGCGCGCGC 81
|||
DB 61 CATCGTCGAGTCGCGCGCGCGC 81

RESULT 8
ABK10711/c
ID ABK10711 standard; DNA; 81 BP.

XX AC ABK10711;
XX DT 05-JUN-2002 (first entry)

XX DE Artificial DNA sequence #3.

XX KM Plastidic phosphoglucomutase; transgenic; plant; gene; ds.

XX OS Synthetic.

FH Key Location/Qualifiers
FT CDS 7..36
FT /*tag= a
FT /product= "ELVISLIVES peptide"
FT /partial
FT /note= "No start or stop codon shown"
FT 44..73
FT /*tag= b
FT /product= "ELVISLIVES peptide"
FT /partial
FT /note= "No start or stop codon shown"

XX PN EP1174510-A2.

XX PD 23-JAN-2002.

XX PF 17-JUL-2001; 2001EP-00306143.

XX PR 17-JUL-2000; 2000US-0218712P.

XX PA (DUPO) DU PONT DE NEMOURS & CO E I.

PI Allen SM, Butler KH, Carlson TV, Ilag IL;
XX WPI; 2002-156692/21.
DR P-PSDB; AAU77109.

XX PT Novel isolated polypeptides having phosphoglucomutase activity and
PT polynucleotides encoding the polypeptides, useful for producing
PT transgenic plants with altered plastidic phosphoglucomutase protein
PT levels.

XX PS Example 9; Page 19; 27pp; English.

CC The invention relates to plastidic phosphoglucomutase polypeptides and
CC their related nucleic acids. The sequences are useful for producing a
CC transgenic plant, by transforming a plant cell with a polynucleotide of
CC the invention and regenerating a plant from the transformed plant cell.
CC Polynucleotide fragments are useful for suppressing the level of
CC expression of a gene encoding a polypeptide having plastidic
CC phosphoglucomutase activity. An isolated polynucleotide that affects the
CC level of expression of a plastidic phosphoglucomutase polypeptide in a
CC plant cell can be identified by introducing a DNA fragment comprising at
CC least 541 nucleotides, measuring the level of the polypeptide in the
CC plant cell containing the polynucleotide, and comparing the level of the
CC polypeptide in the plant cell containing the isolated polynucleotide with
CC the level of the polypeptide in a plant cell that does not contain the
CC isolated polynucleotide. A method for altering the level of expression of
CC a plastidic phosphoglucomutase protein in a host cell comprises
CC transforming a host cell with a chimeric gene and growing the transformed
CC cell under conditions that are suitable for expression of the chimeric
CC gene, where the expression of the gene results in production of altered
CC levels of plastidic phosphoglucomutase. This sequence represents an
CC artificial DNA used for plasmid construction, in the methods of the
CC invention

CC Sequence 81 BP; 8 A; 28 C; 29 G; 16 T; 0 U; 0 Other;

Query Match 52.6%; Score 81; DB 6; Length 81;
Best Local Similarity 100.0%; Pred. No. 1.3e-10;
Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 74 GCGGCCGCGACTCGACGATGAGCGAGATGACCACTCCGCGCGCACTCGACGATGAG 133
|||
DB 81 GCGGCCGCGCGACTCGACGATGAGCGAGATGACCACTCCGCGCGCACTCGACGATGAG 22

OY 134 CGAGATGACCACTCCGCGCG 154
|||
DB 21 CGAGATGACCACTCCGCGCG 1

RESULT 9
AAD29230
ID AAD29230 standard; DNA; 80 BP.

XX AC AAD29230;

XX DT 07-MAY-2002 (first entry)

XX DE Plasmids pKS106, pKS124 1X ELVISLIVES complementary repeat DNA.

XX KM Recombinant construct; gene expression; plasmid pKS124; plasmid pKS106;
XX ds.

XX OS Unidentified.

FH Key Location/Qualifiers
FT CDS 7..36
FT /*tag= a
FT /product= "ELVISLIVES protein"
FT complement(45..74)
FT /*tag= b
FT /product= "ELVISLIVES protein"

XX PN WO200200904-A2.

```
XX 03-JAN-2002.
PD
XX
XX 22-JUN-2001; 2001WO-US019962.
PF
XX
XX 23-JUN-2000; 2000US-0213961P.
PR
XX
XX (DUPO ) DU PONT DE NEMOURS & CO E I.
PA (PION-) PIONEER HI-BRED INT INC.
XX
XX
PI Glassman KF, Gordon-Kamm WJ, Kinney AJ, Lowe K, Stecca KL;
PI Nichols SE;
XX
DR WPI; 2002-139927/18.
DR P-PSDB; AAE18333.
XX
XX
PT New recombinant construct having a promoter operably linked to a DNA
PT sequence which when expressed produces an RNA having homology to a target
PT mRNA and its reverse complement unrelated to endogenous DNA, for reducing
PT gene expression.
XX
XX
PS Claim 45; Page 37; 77pp; English.
XX
XX
CC The present invention relates to a new recombinant construct. The
CC construct comprises a promoter operably linked to a DNA sequence which
CC when expressed by a host produces an RNA having homology to at least one
CC target mRNA expressed by the host and complementary RNA regions. The
CC recombinant construct is useful for reducing the expression of a target
CC mRNA or any similar endogenous mRNA. The RNAs expressed from the
CC recombinant constructs are also used in reducing expression of a target
CC mRNA or any similar endogenous mRNA. The sequences and their reverse
CC complements can be used to reduce the expression of any endogenous
CC genomic sequence that shares substantial similarity to nucleic acid
CC fragment which is in proximity to the DNA or RNA sequence derived from
CC it. The present sequence is 1X ELVISLIVES complementary repeat region DNA
CC found in plasmids pKS106 and pKS124 used in the exemplification of the
CC invention
XX
XX
SQ Sequence 80 BP; 12 A; 28 C; 28 G; 12 T; 0 U; 0 Other;
XX
XX
Query Match 51.9%; Score 80; DB 6; Length 80;
Best Local Similarity 100.0%; Pred. No. 2.2e-10;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
OY 38 CGGCCGAGCTGTCATCTCGCTCATCTCGAGTCGGCGCGCCGCGACTCGACGATGAGC 97
DB 1 CGGCCGAGCTGTCATCTCGCTCATCTCGAGTCGGCGCGCCGCGACTCGACGATGAGC 60
OY 98 GAGATGACCACTCCGCGCG 117
DB 61 GAGATGACCACTCCGCGCG 80
XX
XX
RESULT 10
AAD29230/c
ID AAD29230 standard; DNA; 80 BP.
XX
XX AAD29230;
AC
XX
DT 07-MAY-2002 (first entry)
XX
DE Plasmids pKS106, pKS124 1X ELVISLIVES complementary repeat DNA.
XX
XX Recombinant construct; gene expression; plasmid pKS124; plasmid pKS106;
XX ds.
XX
XX Unidentified.
OS
XX
XX Key Location/Qualifiers
FH CDS 7..36
FT CDS /tag= a
FT CDS /product= "ELVISLIVES protein"
XX CDS complement(45..74)
```

```
PT /*tag= b
FT /product= "ELVISLIVES protein"
XX
XX WO200200904-A2.
PN
XX
XX 03-JAN-2002.
PD
XX
XX 22-JUN-2001; 2001WO-US019962.
PF
XX
XX 23-JUN-2000; 2000US-0213961P.
PR
XX
XX (DUPO ) DU PONT DE NEMOURS & CO E I.
PA (PION-) PIONEER HI-BRED INT INC.
XX
XX
PI Glassman KF, Gordon-Kamm WJ, Kinney AJ, Lowe K, Stecca KL;
PI Nichols SE;
XX
XX
DR WPI; 2002-139927/18.
DR P-PSDB; AAE18333.
XX
XX
XX
XX
PT New recombinant construct having a promoter operably linked to a DNA
PT sequence which when expressed produces an RNA having homology to a target
PT mRNA and its reverse complement unrelated to endogenous DNA, for reducing
PT gene expression.
XX
XX
PS Claim 45; Page 37; 77pp; English.
XX
XX
XX
XX
CC The present invention relates to a new recombinant construct. The
CC construct comprises a promoter operably linked to a DNA sequence which
CC when expressed by a host produces an RNA having homology to at least one
CC target mRNA expressed by the host and complementary RNA regions. The
CC recombinant construct is useful for reducing the expression of a target
CC mRNA or any similar endogenous mRNA. The RNAs expressed from the
CC recombinant constructs are also used in reducing expression of a target
CC mRNA or any similar endogenous mRNA. The sequences and their reverse
CC complements can be used to reduce the expression of any endogenous
CC genomic sequence that shares substantial similarity to nucleic acid
CC fragment which is in proximity to the DNA or RNA sequence derived from
CC it. The present sequence is 1X ELVISLIVES complementary repeat region DNA
CC found in plasmids pKS106 and pKS124 used in the exemplification of the
CC invention
XX
XX
SQ Sequence 80 BP; 12 A; 28 C; 28 G; 12 T; 0 U; 0 Other;
XX
XX
Query Match 51.9%; Score 80; DB 6; Length 80;
Best Local Similarity 100.0%; Pred. No. 2.2e-10;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
OY 38 CGGCCGAGCTGTCATCTCGCTCATCTCGAGTCGGCGCGCCGCGACTCGACGATGAGC 97
DB 80 CGGCCGAGCTGTCATCTCGCTCATCTCGAGTCGGCGCGCCGCGACTCGACGATGAGC 21
OY 98 GAGATGACCACTCCGCGCG 117
DB 20 GAGATGACCACTCCGCGCG 1
XX
XX
RESULT 11
AAD32907
ID AAD32907 standard; DNA; 80 BP.
XX
XX AAD32907;
AC
XX
DT 01-JUL-2002 (first entry)
XX
DE Plasmids pKS106, pKS124 1X ELVISLIVES complementary repeat DNA.
XX
XX Diverged delta-9 fatty acid desaturase; enzyme; cellular lipid; oil;
XX transgenic plant; gene mapping; immunisation; plasmid pKS124;
XX plasmid pKS106; gene; ds.
XX
XX Unidentified.
OS
XX
```

```

FH Key Location/Qualifiers
FT CDS 7..36
FT /*tag= a
FT /product= "ELVISLIVES protein"
FT CDS complement(45..74)
FT /*tag= b
FT /product= "ELVISLIVES protein"
XX
XX WO200216565-A2.
XX
XX 28-FEB-2002.
XX
XX 22-AUG-2001; 2001WO-US026246.
XX
XX 22-AUG-2000; 2000US-0226996P.
XX
XX (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
XX Booth JR, Cahoon RE, Hiltz WD, Kinney AJ, Yadav NS;
XX
XX WPI; 2002-269353/31.
XX
XX P-PSDB; AAE20554.
XX
XX
XX PT New delta-9 fatty acid desaturase polypeptides and polynucleotides,
XX PT useful in creating transgenic plants having altered levels of mono-, poly
XX PT - and unsaturated fatty acids and in increasing the unsaturation levels
XX PT in cellular lipids.
XX
XX PS Example 9; Page 43; 77pp; English.
XX
XX CC The present invention relates to diverged delta-9 fatty acid desaturase
XX CC proteins and polynucleotides encoding such proteins. The nucleic acid
XX CC sequences may be used to increase the level of unsaturation in cellular
XX CC lipids, including oil, in tissues when the enzyme is absent or rate-
XX CC limiting, to isolate cDNAs and genes encoding homologous proteins from
XX CC the same or other plant species and to create transgenic plants in which
XX CC the polypeptides are present at higher or lower levels than normal or in
XX CC cell types or developmental stages in which they are not normally found,
XX CC thus altering the level of mono-, poly- and unsaturated fatty acids in
XX CC those cells. They are useful as probes for genetic and physical gene
XX CC mapping and as markers, e.g. restriction fragment length polymorphism
XX CC (RFLP) markers. The peptides can be used to immunise animals to produce
XX CC antibodies specific for the peptides and proteins. The present sequence
XX CC is 1X ELVISLIVES complementary repeat region DNA found in plasmids PKS106
XX CC and PKS124. This sequence is used in the exemplification of the invention
XX CC for the suppression of Fad2 in soybean
XX
XX SQ Sequence 80 BP; 12 A; 28 C; 28 G; 12 T; 0 U; 0 Other;
XX
XX Query Match 51.9%; Score 80; DB 6; Length 80;
XX Best Local Similarity 100.0%; Pred. No. 2.2e-10;
XX Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 38 CGGCCGAGCTGTCATCTCGTCATCTCGAGTCGGCGCCGCCGACTCGACGATGAGC 97
XX ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
XX Db 1 CGGCCGAGCTGTCATCTCGTCATCTCGAGTCGGCGCCGCCGACTCGACGATGAGC 60
XX
XX QY 98 GAGATGACCACTCCGCCG.117
XX ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
XX Db 61 GAGATGACCACTCCGCCG 80
XX
XX RESULT 12
XX AAD32907/c
XX ID AAD32907 standard; DNA; 80 BP.
XX
XX AC AAD32907;
XX
XX XX 01-JUL-2002 (first entry)
XX
XX DT Plasmids PKS106, PKS124 1X ELVISLIVES complementary repeat DNA.
XX
XX DE Plasmids PKS106, PKS124 1X ELVISLIVES complementary repeat DNA.
XX
XX XX Diverged delta-9 fatty acid desaturase; enzyme; cellular lipid; oil;
XX
XX KW
```

```

KW transgenic plant; gene mapping; immunisation; plasmid PKS124;
KW plasmid PKS106; gene; ds.
XX
XX Unidentified.
XX
XX FH Key Location/Qualifiers
XX FT CDS 7..36
XX FT /*tag= a
XX FT /product= "ELVISLIVES protein"
XX FT complement(45..74)
XX FT /*tag= b
XX FT /product= "ELVISLIVES protein"
XX
XX XX WO200216565-A2.
XX
XX XX 28-FEB-2002.
XX
XX XX 22-AUG-2001; 2001WO-US026246.
XX
XX XX 22-AUG-2000; 2000US-0226996P.
XX
XX XX (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
XX XX Booth JR, Cahoon RE, Hiltz WD, Kinney AJ, Yadav NS;
XX
XX XX WPI; 2002-269353/31.
XX
XX XX P-PSDB; AAE20554.
XX
XX
XX PT New delta-9 fatty acid desaturase polypeptides and polynucleotides,
XX PT useful in creating transgenic plants having altered levels of mono-, poly
XX PT - and unsaturated fatty acids and in increasing the unsaturation levels
XX PT in cellular lipids.
XX
XX PS Example 9; Page 43; 77pp; English.
XX
XX CC The present invention relates to diverged delta-9 fatty acid desaturase
XX CC proteins and polynucleotides encoding such proteins. The nucleic acid
XX CC sequences may be used to increase the level of unsaturation in cellular
XX CC lipids, including oil, in tissues when the enzyme is absent or rate-
XX CC limiting, to isolate cDNAs and genes encoding homologous proteins from
XX CC the same or other plant species and to create transgenic plants in which
XX CC the polypeptides are present at higher or lower levels than normal or in
XX CC cell types or developmental stages in which they are not normally found,
XX CC thus altering the level of mono-, poly- and unsaturated fatty acids in
XX CC those cells. They are useful as probes for genetic and physical gene
XX CC mapping and as markers, e.g. restriction fragment length polymorphism
XX CC (RFLP) markers. The peptides can be used to immunise animals to produce
XX CC antibodies specific for the peptides and proteins. The present sequence
XX CC is 1X ELVISLIVES complementary repeat region DNA found in plasmids PKS106
XX CC and PKS124. This sequence is used in the exemplification of the invention
XX CC for the suppression of Fad2 in soybean
XX
XX SQ Sequence 80 BP; 12 A; 28 C; 28 G; 12 T; 0 U; 0 Other;
XX
XX Query Match 51.9%; Score 80; DB 6; Length 80;
XX Best Local Similarity 100.0%; Pred. No. 2.2e-10;
XX Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 38 CGGCCGAGCTGTCATCTCGTCATCTCGAGTCGGCGCCGCCGACTCGACGATGAGC 97
XX ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
XX Db 80 CGGCCGAGCTGTCATCTCGTCATCTCGAGTCGGCGCCGCCGACTCGACGATGAGC 21
XX
XX QY 98 GAGATGACCACTCCGCCG 117
XX ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
XX Db 20 GAGATGACCACTCCGCCG 1
XX
XX RESULT 13
XX ABK10712
XX ID ABK10712 standard; DNA; 92 BP.
XX
XX AC ABK10712;
XX
XX XX
```

```
DT 05-JUN-2002 (first entry)
XX
XX Artificial DNA sequence #4.
DE
XX
XX Plastidic phosphoglucomutase; transgenic; plant; gene; ss.
XX
OS Synthetic.
XX
PN EP1174510-A2.
XX
XX 23-JAN-2002.
PD
XX
XX 17-JUL-2001; 2001EP-00306143.
PF
XX
XX 17-JUL-2000; 2000US-0218712P.
PR
XX
XX (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
XX Allen SM, Butler KH, Carlson TJ, Ilag LL;
PI
XX WPI; 2002-156692/21.
DR
XX
XX Novel isolated polypeptides having phosphoglucomutase activity and
PT polynucleotides encoding the polypeptides, useful for producing
PT transgenic plants with altered plastidic phosphoglucomutase protein
PT levels.
XX
XX Example 9; Page 19; 27pp; English.
PS
XX The invention relates to plastidic phosphoglucomutase polypeptides and
XX their related nucleic acids. The sequences are useful for producing a
CC transgenic plant, by transforming a plant cell with a polynucleotide of
CC the invention and regenerating a plant from the transformed plant cell.
CC Polynucleotide fragments are useful for suppressing the level of
CC expression of a gene encoding a polypeptide having plastidic
CC phosphoglucomutase activity. An isolated polynucleotide that affects the
CC level of expression of a plastidic phosphoglucomutase polypeptide in a
CC plant cell can be identified by introducing a DNA fragment comprising at
CC least 541 nucleotides, measuring the level of the polypeptide in the
CC plant cell containing the polynucleotide, and comparing the level of the
CC polypeptide in the plant cell containing the isolated polynucleotide with
CC the level of the polypeptide in a plant cell that does not contain the
CC isolated polynucleotide. A method for altering the level of expression of
CC a plastidic phosphoglucomutase protein in a host cell comprises
CC transforming a host cell with a chimeric gene and growing the transformed
CC cell under conditions that are suitable for expression of the chimeric
CC gene, where the expression of the gene results in production of altered
CC levels of plastidic phosphoglucomutase. This sequence represents an
CC artificial DNA used for plasmid construction, in the methods of the
CC invention
XX
XX
SQ Sequence 92 BP; 16 A; 30 C; 30 G; 16 T; 0 U; 0 Other;
Query Match 51.9%; Score 80; DB 6; Length 92;
Best Local Similarity 100.0%; Pred. No. 2.2e-10;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 38 CGGCCGAGCTGGTCACTCGCTCATGCTGAGTCGGCGCGCCGCGACTCGACGATGAGC 97
DB 7 CGGCCGAGCTGGTCACTCGCTCATGCTGAGTCGGCGCGCCGCGACTCGACGATGAGC 66
OY 98 GAGATGACCAAGCTCCGGCCG 117
DB 67 GAGATGACCAAGCTCCGGCCG 86
```

```
RESULT 14
ABK10712/C
ID ABK10712 standard; DNA; 92 BP.
XX
XX ABK10712;
AC
XX
DT 05-JUN-2002 (first entry)
```

```
XX
XX Artificial DNA sequence #4.
DE
XX
XX Plastidic phosphoglucomutase; transgenic; plant; gene; ss.
XX
OS Synthetic.
XX
PN EP1174510-A2.
XX
XX 23-JAN-2002.
PD
XX
XX 17-JUL-2001; 2001EP-00306143.
PF
XX
XX 17-JUL-2000; 2000US-0218712P.
PR
XX
XX (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
XX Allen SM, Butler KH, Carlson TJ, Ilag LL;
PI
XX WPI; 2002-156692/21.
DR
XX
XX Novel isolated polypeptides having phosphoglucomutase activity and
PT polynucleotides encoding the polypeptides, useful for producing
PT transgenic plants with altered plastidic phosphoglucomutase protein
PT levels.
XX
XX Example 9; Page 19; 27pp; English.
PS
XX The invention relates to plastidic phosphoglucomutase polypeptides and
XX their related nucleic acids. The sequences are useful for producing a
CC transgenic plant, by transforming a plant cell with a polynucleotide of
CC the invention and regenerating a plant from the transformed plant cell.
CC Polynucleotide fragments are useful for suppressing the level of
CC expression of a gene encoding a polypeptide having plastidic
CC phosphoglucomutase activity. An isolated polynucleotide that affects the
CC level of expression of a plastidic phosphoglucomutase polypeptide in a
CC plant cell can be identified by introducing a DNA fragment comprising at
CC least 541 nucleotides, measuring the level of the polypeptide in the
CC plant cell containing the polynucleotide, and comparing the level of the
CC polypeptide in the plant cell containing the isolated polynucleotide with
CC the level of the polypeptide in a plant cell that does not contain the
CC isolated polynucleotide. A method for altering the level of expression of
CC a plastidic phosphoglucomutase protein in a host cell comprises
CC transforming a host cell with a chimeric gene and growing the transformed
CC cell under conditions that are suitable for expression of the chimeric
CC gene, where the expression of the gene results in production of altered
CC levels of plastidic phosphoglucomutase. This sequence represents an
CC artificial DNA used for plasmid construction, in the methods of the
CC invention
XX
XX
SQ Sequence 92 BP; 16 A; 30 C; 30 G; 16 T; 0 U; 0 Other;
Query Match 51.9%; Score 80; DB 6; Length 92;
Best Local Similarity 100.0%; Pred. No. 2.2e-10;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 38 CGGCCGAGCTGGTCACTCGCTCATGCTGAGTCGGCGCGCCGCGACTCGACGATGAGC 97
DB 86 CGGCCGAGCTGGTCACTCGCTCATGCTGAGTCGGCGCGCCGCGACTCGACGATGAGC 27
OY 98 GAGATGACCAAGCTCCGGCCG 117
DB 26 GAGATGACCAAGCTCCGGCCG 7
```

```
RESULT 15
AAD29232
ID AAD29232 standard; DNA; 92 BP.
XX
XX AAD29232;
AC
XX
DT 07-MAY-2002 (first entry)
```

DE ELVISLIVES complementary region DNA amplifying PCR primer #1.
XX
XX Recombinant construct; gene expression; PCR primer; ss.
XX
OS Unidentified.
XX
PN WO200200904-A2.
XX
PD 03-JAN-2002.
XX
PF 22-JUN-2001; 2001WO-US019962.
XX
PR 23-JUN-2000; 2000US-0213961P.
XX
PA (DUPO) DU PONT DE NEMOURS & CO E I.
PA (PION-) PIONEER HI-BRED INT INC.
PI Glassman KF, Gordon-Kamm WJ, Kinney AJ, Lowe K, Stecca KL;
PI Nichols SE;
XX
DR WPI; 2002-139927/18.
XX
PT New recombinant construct having a promoter operably linked to a DNA
PT sequence which when expressed produces an RNA having homology to a target
PT mRNA and its reverse complement unrelated to endogenous DNA, for reducing
PT gene expression.
XX
PS Example 7; Page 37; 77pp; English.
XX
CC The present invention relates to a new recombinant construct. The
CC construct comprises a promoter operably linked to a DNA sequence which
CC when expressed by a host produces an RNA having homology to at least one
CC target mRNA expressed by the host and complementary RNA regions. The
CC recombinant construct is useful for reducing the expression of a target
CC mRNA or any similar endogenous mRNA. The RNAs expressed from a target
CC recombinant constructs are also used in reducing expression of a target
CC mRNA or any similar endogenous mRNA. The sequences and their reverse
CC complements can be used to reduce the expression of any endogenous
CC genomic sequence that shares substantial similarity to nucleic acid
CC fragment which is in proximity to the DNA or RNA sequence derived from
CC it. The present sequence is a PCR primer used for amplifying ELVISLIVES
CC complementary region DNA used in the exemplification of the invention
XX
SQ Sequence 92 BP; 16 A; 30 C; 30 G; 16 T; 0 U; 0 Other;
XX
Query Match 51.9%; Score 80; DB 6; Length 92;
Best Local Similarity 100.0%; Pred. No. 2.2e-10;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 38 CGGCCGAGCTGTGTCATCTCGCTCATCTCGAGTCGGCGCGCCGACTCGACGATGAGC 97
Db 7 CGGCCGAGCTGTGTCATCTCGCTCATCTCGAGTCGGCGCGCCGACTCGACGATGAGC 66
QY 98 GAGATGACCACTCCGGCCG 117
Db 67 GAGATGACCACTCCGGCCG 86

RESULT 16
AAD29232/C
ID AAD29232 standard; DNA; 92 BP.
XX
AC AAD29232;
XX
DT 07-MAY-2002 (first entry)
XX
DE ELVISLIVES complementary region DNA amplifying PCR primer #1.
XX
KW Recombinant construct; gene expression; PCR primer; ss.
OS Unidentified.
XX
PN WO200200904-A2.

XX
PD 03-JAN-2002.
XX
PF 22-JUN-2001; 2001WO-US019962.
XX
PR 23-JUN-2000; 2000US-0213961P.
XX
PA (DUPO) DU PONT DE NEMOURS & CO E I.
PA (PION-) PIONEER HI-BRED INT INC.
PI Glassman KF, Gordon-Kamm WJ, Kinney AJ, Lowe K, Stecca KL;
PI Nichols SE;
XX
DR WPI; 2002-139927/18.
XX
PT New recombinant construct having a promoter operably linked to a DNA
PT sequence which when expressed produces an RNA having homology to a target
PT mRNA and its reverse complement unrelated to endogenous DNA, for reducing
PT gene expression.
XX
PS Example 7; Page 37; 77pp; English.
XX
CC The present invention relates to a new recombinant construct. The
CC construct comprises a promoter operably linked to a DNA sequence which
CC when expressed by a host produces an RNA having homology to at least one
CC target mRNA expressed by the host and complementary RNA regions. The
CC recombinant construct is useful for reducing the expression of a target
CC mRNA or any similar endogenous mRNA. The RNAs expressed from the
CC recombinant constructs are also used in reducing expression of a target
CC mRNA or any similar endogenous mRNA. The sequences and their reverse
CC complements can be used to reduce the expression of any endogenous
CC genomic sequence that shares substantial similarity to nucleic acid
CC fragment which is in proximity to the DNA or RNA sequence derived from
CC it. The present sequence is a PCR primer used for amplifying ELVISLIVES
CC complementary region DNA used in the exemplification of the invention
XX
SQ Sequence 92 BP; 16 A; 30 C; 30 G; 16 T; 0 U; 0 Other;
XX
Query Match 51.9%; Score 80; DB 6; Length 92;
Best Local Similarity 100.0%; Pred. No. 2.2e-10;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 38 CGGCCGAGCTGTGTCATCTCGCTCATCTCGAGTCGGCGCGCCGACTCGACGATGAGC 97
Db 86 CGGCCGAGCTGTGTCATCTCGCTCATCTCGAGTCGGCGCGCCGACTCGACGATGAGC 27
QY 98 GAGATGACCACTCCGGCCG 117
Db 26 GAGATGACCACTCCGGCCG 7

RESULT 17
ABK10710
ID ABK10710 standard; DNA; 44 BP.
XX
AC ABK10710;
XX
DT 05-JUN-2002 (first entry)
XX
DE Artificial DNA sequence #2.
XX
KM Plasmidic phosphoglucumutase; transgenic; plant; gene; ds.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FH CDS 7..36
FT /*tag= a
FT /product= "ELVISLIVES peptide"
FT /partial
FT /note= "No start or stop codon shown"
XX
PN BP1174510-A2.

XX 23-JAN-2002.
PD 17-JUL-2001; 2001EP-00306143.
XX 17-JUL-2000; 2000US-0218712P.
PR (DUPO) DU PONT DE NEMOURS & CO E I.
XX Allen SM, Butler KH, Carlson TJ, Ilag LL;
PI WPI; 2002-156692/21.
DR P-PSDB; AAU77109.
XX
PT Novel isolated polypeptides having phosphoglucomutase activity and
PT polynucleotides encoding the polypeptides, useful for producing
PT transgenic plants with altered plastidic phosphoglucomutase protein
PT levels.
XX
PS Example 9; Page 19; 27pp; English.
XX
CC The invention relates to plastidic phosphoglucomutase polypeptides and
CC their related nucleic acids. The sequences are useful for producing a
CC transgenic plant, by transforming a plant cell with a polynucleotide of
CC the invention and regenerating a plant from the transformed plant cell.
CC Polynucleotide fragments are useful for suppressing the level of
CC expression of a gene encoding a polypeptide having plastidic
CC phosphoglucomutase activity. An isolated polynucleotide that affects the
CC level of expression of a plastidic phosphoglucomutase polypeptide in a
CC plant cell can be identified by introducing a DNA fragment comprising at
CC least 541 nucleotides, measuring the level of the polypeptide in the
CC plant cell containing the polynucleotide, and comparing the level of the
CC polypeptide in the plant cell containing the isolated polynucleotide with
CC the level of the polypeptide in a plant cell that does not contain the
CC isolated polynucleotide. A method for altering the level of expression of
CC a plastidic phosphoglucomutase protein in a host cell comprises
CC transforming a host cell with a chimeric gene and growing the transformed
CC cell under conditions that are suitable for expression of the chimeric
CC gene, where the expression of the gene results in production of altered
CC levels of plastidic phosphoglucomutase. This sequence represents an
CC artificial DNA used for plasmid construction, in the methods of the
CC invention
XX
SQ Sequence 44 BP; 4 A; 16 C; 16 G; 8 T; 0 U; 0 Other;

Query Match 28.6%; Score 44; DB 6; Length 44;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 CGGCCGAGCTGTCATCTCGCTCATCGTCGAGTCGGCGCGCC 81
Db 1 CGGCCGAGCTGTCATCTCGCTCATCGTCGAGTCGGCGCGCC 44

RESULT 18
ABK10710/c
ID ABK10710 standard; DNA; 44 BP.
XX
AC ABK10710;
XX
DT 05-JUN-2002 (first entry)
XX
DE Artificial DNA sequence #2.
XX
KW Plastidic phosphoglucomutase; transgenic; plant; gene; ds.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT 7.36
FT /tag= a
FT /product= "ELVISLIVES peptide"
FT /partial

FT /note= "No start or stop codon shown"
XX
PN EP1174510-A2.
XX 23-JAN-2002.
PD 17-JUL-2001; 2001EP-00306143.
XX 17-JUL-2000; 2000US-0218712P.
PR (DUPO) DU PONT DE NEMOURS & CO E I.
XX Allen SM, Butler KH, Carlson TJ, Ilag LL;
PI WPI; 2002-156692/21.
DR P-PSDB; AAU77109.
XX
PT Novel isolated polypeptides having phosphoglucomutase activity and
PT polynucleotides encoding the polypeptides, useful for producing
PT transgenic plants with altered plastidic phosphoglucomutase protein
PT levels.
XX
PS Example 9; Page 19; 27pp; English.
XX
CC The invention relates to plastidic phosphoglucomutase polypeptides and
CC their related nucleic acids. The sequences are useful for producing a
CC transgenic plant, by transforming a plant cell with a polynucleotide of
CC the invention and regenerating a plant from the transformed plant cell.
CC Polynucleotide fragments are useful for suppressing the level of
CC expression of a gene encoding a polypeptide having plastidic
CC phosphoglucomutase activity. An isolated polynucleotide that affects the
CC level of expression of a plastidic phosphoglucomutase polypeptide in a
CC plant cell can be identified by introducing a DNA fragment comprising at
CC least 541 nucleotides, measuring the level of the polypeptide in the
CC plant cell containing the polynucleotide, and comparing the level of the
CC polypeptide in the plant cell containing the isolated polynucleotide with
CC the level of the polypeptide in a plant cell that does not contain the
CC isolated polynucleotide. A method for altering the level of expression of
CC a plastidic phosphoglucomutase protein in a host cell comprises
CC transforming a host cell with a chimeric gene and growing the transformed
CC cell under conditions that are suitable for expression of the chimeric
CC gene, where the expression of the gene results in production of altered
CC levels of plastidic phosphoglucomutase. This sequence represents an
CC artificial DNA used for plasmid construction, in the methods of the
CC invention
XX
SQ Sequence 44 BP; 4 A; 16 C; 16 G; 8 T; 0 U; 0 Other;

Query Match 28.6%; Score 44; DB 6; Length 44;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 74 GCGGCCGCGACTCGACGATGAGCGAGATGACCACTCCGCGC 117
Db 44 GCGGCCGCGACTCGACGATGAGCGAGATGACCACTCCGCGC 1

RESULT 19
AAC89216
ID AAC89216 standard; DNA; 194 BP.
XX
AC AAC89216;
XX
DT 07-MAR-2001 (first entry)
XX
DE Human brain T calcium channel alpha 1G subunit gene exon 16.
XX
KW Ion channel; human; brain T calcium channel; alpha 1G subunit;
KW alpha 1I subunit; epilepsy; drug screening; ds.
XX
OS Homo sapiens.
XX
PN WO200070044-A2.

XX 23-NOV-2000.
 PD 08-MAY-2000; 2000WO-US012383.
 XX
 PF 13-MAY-1999; 99US-0134063P.
 PR 04-JUN-1999; 99US-0137547P.
 XX
 PA (UYJO) UNIV JOHNS HOPKINS.
 XX
 PI Miltman S, Agnew WS;
 XX
 DR WPI; 2001-031928/04.
 DR P-PSDB; AAB50116.
 XX
 PT Splice variants of the human brain T calcium channel alpha 1G and alpha
 PT 1I subunits and genes encoding the subunits, useful as targets for
 PT antiepileptic drugs or for testing compounds or compositions useful in
 PT treating epilepsy.
 XX
 PS Claim 5; Page 19; 89pp; English.
 XX
 CC The present invention provides the protein and coding sequences for the
 CC human brain T calcium channel alpha 1G and alpha 1I subunits. The alpha
 CC 1G subunit gene (designated CACNA1G) consists of 38 exons, and
 CC alternative processing leads to the production of 64 different proteins.
 CC The alpha 1I subunit (designated CACNA1I) consists of 37 exons, and 8
 CC proteins are produced due to alternative processing. The sequences
 CC provided by the invention are useful for screening drugs for use in the
 CC treatment of epilepsy
 XX
 SQ Sequence 194 BP; 33 A; 72 C; 67 G; 22 T; 0 U; 0 Other;
 XX
 QY Query Match 19.1%; Score 29.4; DB 4; Length 194;
 Best Local Similarity 58.6%; Pred. No. 4.2e+02;
 Matches 51; Conservative 0; Mismatches 36; Indels 0; Gaps 0;
 Db 30 CGAGTCGGCGCGGAGCTGTGTCATCTCGCTCATCTGCGAGTCGGCGCGCGGCGGACTCGA 89
 22 CGAGCTGCGGAGAGAGCTGCTGCGCGCTCTCATCTCATCCACGCGCGGCGGACCCATGT 81
 QY 90 CGATGAGCGAGATGACCACTCCGCC 116
 82 CGCTGCCCAAGAGCAACGACGCGGCC 108
 Db
 RESULT 20
 AAC89216/c
 ID AAC89216 standard; DNA; 194 BP.
 XX
 AC AAC89216;
 XX
 DT 07-MAR-2001 (first entry)
 XX
 DE Human brain T calcium channel alpha 1G subunit gene exon 16.
 XX
 KW Ion channel; human; brain T calcium channel; alpha 1G subunit;
 KW alpha 1I subunit; epilepsy; drug screening; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200070044-A2.
 XX
 PD 23-NOV-2000.
 XX
 PF 08-MAY-2000; 2000WO-US012383.
 XX
 PR 13-MAY-1999; 99US-0134063P.
 PR 04-JUN-1999; 99US-0137547P.
 XX
 PA (UYJO) UNIV JOHNS HOPKINS.
 XX
 PI Miltman S, Agnew WS;

XX WPI; 2001-031928/04.
 DR P-PSDB; AAB50116.
 XX
 PT Splice variants of the human brain T calcium channel alpha 1G and alpha
 PT 1I subunits and genes encoding the subunits, useful as targets for
 PT antiepileptic drugs or for testing compounds or compositions useful in
 PT treating epilepsy.
 XX
 PS Claim 5; Page 19; 89pp; English.
 XX
 CC The present invention provides the protein and coding sequences for the
 CC human brain T calcium channel alpha 1G and alpha 1I subunits. The alpha
 CC 1G subunit gene (designated CACNA1G) consists of 38 exons, and
 CC alternative processing leads to the production of 64 different proteins.
 CC The alpha 1I subunit (designated CACNA1I) consists of 37 exons, and 8
 CC proteins are produced due to alternative processing. The sequences
 CC provided by the invention are useful for screening drugs for use in the
 CC treatment of epilepsy
 XX
 SQ Sequence 194 BP; 33 A; 72 C; 67 G; 22 T; 0 U; 0 Other;
 XX
 QY Query Match 19.1%; Score 29.4; DB 4; Length 194;
 Best Local Similarity 58.6%; Pred. No. 4.2e+02;
 Matches 51; Conservative 0; Mismatches 36; Indels 0; Gaps 0;
 Db 39 GCGCGGAGCTGTGTCATCTCGCTCATCTGCGAGTCGGCGCGCGGCGGACTGAGCG 98
 108 GGCCCTGTGCTGTGCTCTTGCGGACGACATGGGTGTGCGCGCGGTGTGATGATGAGAG 49
 QY 99 AGATGACCACTCCGCGCGGCGACTCG 125
 48 GCGGACAGAGGCTCTTCCGAGCTCCG 22
 Db
 RESULT 21
 ABX88193
 ID ABX88193 standard; cDNA; 197 BP.
 XX
 AC ABX88193;
 XX
 DT 24-APR-2003 (first entry)
 XX
 DE Corn ear-derived polynucleotide (cpd) #6653.
 XX
 KW Corn ear-derived polynucleotide; cdp; cDNA library; SATMON022; SATMON023;
 KW structural gene; functional gene; regulatory gene;
 KW corn ear-specific profile; gene transcription; gene expression;
 KW hybrid plant; desirable trait expression; plant breeding program;
 KW inheritance; desired characteristic; growth; development;
 KW disease resistance; environmental adaptability; quality; yield;
 KW multigene trait; plant; gene; ss.
 XX
 OS Zea mays.
 XX
 PN US6476212-B1.
 XX
 PD 05-NOV-2002.
 XX
 PF 14-MAY-1999; 99US-00313294.
 XX
 PR 26-MAY-1998; 98US-0086722P.
 XX
 PA (INCY-) INCYTE GENOMICS INC.
 XX
 PI lalgudi RV, Ito LY, Sherman BK;
 XX
 DR WPI; 2003-208840/20.
 XX
 PT Novel purified corn-ear derived polynucleotide useful as hybridization
 PT probe for detecting polynucleotide in sample, and for identifying,
 PT evaluating, and altering desired characteristics associated with growth,
 PT development.

XX Example; SEQ ID NO 6653; 390pp; English.
PS
XX The present invention relates to the isolation of corn ear-derived
CC polynucleotides (cdps) from the corn (Zea mays) cDNA libraries SATMON022
CC and SATMON023. Some of the cpds uniquely identify structural, functional,
CC and regulatory genes of corn ear. The polynucleotide sequences are
CC useful for detecting cpds in a sample, for producing a corn ear-specific
CC profile of gene transcription, for detecting altered gene expression in
CC inbred or hybrid plants, and for screening several molecules for specific
CC binding to the polynucleotide. The cpds are useful to identify, isolate,
CC or extend identical or related corn-ear nucleic acid sequences from DNA
CC libraries, and in nucleic acid amplification or hybridisation techniques
CC to follow the expression of desirable traits through plant breeding
CC programs. Preferably, the cpds are used to identify, evaluate, alter, or
CC follow the inheritance of desired characteristics associated with growth
CC and development, disease resistance, environmental adaptability, quality,
CC and yield of corn. The cpds are also useful as molecular markers for
CC studying inheritance and multigene traits in a plant breeding program.
CC The cpds are useful for producing purified corn-ear polypeptides by
CC recombinant techniques. They are also useful in diagnostic assays to
CC detect or confirm conditions or diseases associated with abnormal levels
CC of cdp expression. ABX81541-ABX89140 represent corn ear-derived
CC polynucleotides (cpds) of the invention. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from the USPTO web site at
CC seqdata.uspto.gov/psipSIDEntry.html
XX
SQ Sequence 197 BP; 42 A; 55 C; 68 G; 30 T; 0 U; 2 Other;
Query Match 18.2%; Score 28; DB 10; Length 197;
Best Local Similarity 51.2%; Pred. No. 9.1e+02;
Matches 64; Conservative 0; Mismatches 61; Indels 0; Gaps 0;
OY 28 GTGAGTCGGCGCGCCGAGCTGCTCATCTCGCTCATCTCGAGTCGGCGCGCCGACTC 87
DB 63 GCGCGGTGTCGCCCGCATCTGCTGCGCCGACGAGCTGTTA CTTCTCTCAGTCTC 122
OY 88 GACGATGACGAGATGACACGAGCTCCGCGCGCCGACTCGACGATGAGAGATGACCACT 147
DB 123 AGTCAGAGCAAGATGGTGCCGCGCGCAGATGACCGAGAGAGCGGAGAGACAGA 182
OY 148 CCGGC 152
DB 183 GCAGC 187
RESULT 22
ID ABX88193 standard; cDNA; 197 BP.
XX
AC ABX88193;
XX
DT 24-APR-2003 (first entry)
XX
DE Corn ear-derived polynucleotide (cpd) #6653.
XX
KW Corn ear-derived polynucleotide; cdp, cDNA library; SATMON022; SATMON023;
KW structural gene; functional gene; regulatory gene;
KW corn ear-specific profile; gene transcription; gene expression;
KW hybrid plant; desirable trait expression; plant breeding program;
KW inheritance; desirable characteristic; growth; development;
KW disease resistance; environmental adaptability; quality; yield;
KW multigene trait; plant; gene; ss.
XX
OS Zea mays.
XX
PN US6476212-B1.
XX
PD 05-NOV-2002.
XX
PF 14-MAY-1999; 99US-00313294.
XX

PR 26-MAY-1998; 98US-0086722P.
XX
XX (INCY-) INCYTE GENOMICS INC.
XX
PI Lalgudi RV, Ito LY, Sherman BK;
XX
DR WPI; 2003-208840/20.
XX
PT Novel purified corn-ear derived polynucleotide useful as hybridization
PT probe for detecting polynucleotide in sample, and for identifying,
PT evaluating, and altering desired characteristics associated with growth,
PT development.
XX
XX Example; SEQ ID NO 6653; 390pp; English.
PS
XX The present invention relates to the isolation of corn ear-derived
CC polynucleotides (cdps) from the corn (Zea mays) cDNA libraries SATMON022
CC and SATMON023. Some of the cpds uniquely identify structural, functional,
CC and regulatory genes of corn ear. The polynucleotide sequences are
CC useful for detecting cpds in a sample, for producing a corn ear-specific
CC profile of gene transcription, for detecting altered gene expression in
CC inbred or hybrid plants, and for screening several molecules for specific
CC binding to the polynucleotide. The cpds are useful to identify, isolate,
CC or extend identical or related corn-ear nucleic acid sequences from DNA
CC libraries, and in nucleic acid amplification or hybridisation techniques
CC to follow the expression of desirable traits through plant breeding
CC programs. Preferably, the cpds are used to identify, evaluate, alter, or
CC follow the inheritance of desired characteristics associated with growth
CC and development, disease resistance, environmental adaptability, quality,
CC and yield of corn. The cpds are also useful as molecular markers for
CC studying inheritance and multigene traits in a plant breeding program.
CC The cpds are useful for producing purified corn-ear polypeptides by
CC recombinant techniques. They are also useful in diagnostic assays to
CC detect or confirm conditions or diseases associated with abnormal levels
CC of cdp expression. ABX81541-ABX89140 represent corn ear-derived
CC polynucleotides (cpds) of the invention. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from the USPTO web site at
CC seqdata.uspto.gov/psipSIDEntry.html
XX
SQ Sequence 197 BP; 42 A; 55 C; 68 G; 30 T; 0 U; 2 Other;
Query Match 18.2%; Score 28; DB 10; Length 197;
Best Local Similarity 51.2%; Pred. No. 9.1e+02;
Matches 64; Conservative 0; Mismatches 61; Indels 0; Gaps 0;
OY 3 GCCGAGCTGCTCATCTCGCTCATCTCGAGTCGGCGCGCCGAGCTGCTCATCTCGCTCA 62
DB 187 GCTGCTCTGCTTCTCCCGCTCTCTCTCGTATCTGCGCGCCGACCATCTTGCTCC 128
OY 63 TCGTCAGTCGGCGCGCCGCGACTCGACGATGAGCGAGATGACCACTCCGCGCGGAC 122
DB 127 TGA CTGAGACTGAGAGANGTAACAGCTGCGTGGCGCAGACAGATCGGCGGACACC 68
OY 123 TCGAC 127
DB 67 GCGCC 63
RESULT 23
ID AAL44709 standard; DNA; 156 BP.
XX
AC AAL44709;
XX
DT 03-MAY-2002 (first entry)
XX
DE Human glutamate receptor delta-1 subunit coding sequence SEQ ID NO: 9.
XX
KW Human; glutamate receptor delta-1 subunit; epilepsy; brain damage;
KW neurodegenerative disorder; Huntington's disease; Parkinson's disease;
KW Alzheimer's disease; schizophrenia; mood disorder; dementia;
KW neuropathological pain; pain; receptor; anticonvulsant; nootropic;

KW neuroprotective; vasotropic; analgesic; neuroleptic; cytostatic;
KM uropathic; antiparkinsonian; vulnerary; gene; ds.
OS Homo sapiens.
XX WO200206313-A2.
PN 24-JAN-2002.
XX 13-JUL-2001; 2001WO-EP008102.
PF 18-JUL-2000; 2000US-0218835P.
XX 18-JUL-2000; 2000US-0218835P.
PR (FARB) BAYER AG.
XX Kossida S;
PI WPI; 2002-195800/25.
DR
XX Novel human glutamate receptor delta-1 subunit protein which can be
PT regulated for treating epilepsy, schizophrenia, neurodegenerative
PT diseases, ischemia, pain, benign prostate hyperplasia and urinary
PT incontinence.
XX Claim 19; Fig 9; 97pp; English.
PS
XX The present invention provides a human glutamate receptor delta-1 subunit
CC polypeptide. This can be used to screen for agents which modulate the
CC activity of glutamate receptor delta-1 subunit polypeptide, which may
CC then be used in the treatment of diseases such as epilepsy, brain damage,
CC neurodegenerative disorders such as Alzheimer's disease, Huntington's
CC disease and Parkinson's disease, schizophrenia, mood disorders, pain,
CC neuropathologic pain and dementias. The present sequence is a fragment of
CC the human glutamate receptor delta-1 subunit coding sequence
XX
SQ Sequence 156 BP; 41 A; 45 C; 44 G; 26 T; 0 U; 0 Other;
Query Match 17.3%; Score 26.6; DB 6; Length 156;
Best Local Similarity 60.3%; Pred. No. 2e+03;
Matches 44; Conservative 0; Mismatches 29; Indels 0; Gaps 0;
QY 60 TCATCGTCGAGTCGGCGCGCCGACTCGACGATGACGACGATGACCGACTCCGCCGCC 119
Db 8 TCTTCGAGGAGAACGCGGCCAAGACGACAGGAGTGTTCAGTTGGCGGTATCCGACCTGA 67
QY 120 GACTCGACGATGA 132
Db 68 GCCTCAACGATGA 80
RESULT 24
AAL44709/c
ID AAL44709 standard; DNA; 156 BP.
XX
AC AAL44709;
XX
DT 03-MAY-2002 (first entry)
XX
DE Human glutamate receptor delta-1 subunit coding sequence SEQ ID NO: 9.
XX
KW Human; glutamate receptor delta-1 subunit; epilepsy; brain damage;
KW neurodegenerative disorder; Huntington's disease; Parkinson's disease;
KW Alzheimer's disease; schizophrenia; mood disorder; dementia;
KW neuropathological pain; pain; receptor; anticonvulsant; nootropic;
KW neuroprotective; vasotropic; analgesic; neuroleptic; cytostatic;
KW uropathic; antiparkinsonian; vulnerary; gene; ds.
XX
OS Homo sapiens.
XX
PN WO200206313-A2.
XX
PD 24-JAN-2002.
XX

PF 13-JUL-2001; 2001WO-EP008102.
XX
PR 18-JUL-2000; 2000US-0218835P.
XX
PA (FARB) BAYER AG.
XX
PI Kossida S;
XX
DR WPI; 2002-195800/25.
XX
PT Novel human glutamate receptor delta-1 subunit protein which can be
PT regulated for treating epilepsy, schizophrenia, neurodegenerative
PT diseases, ischemia, pain, benign prostate hyperplasia and urinary
PT incontinence.
XX
PS Claim 19; Fig 9; 97pp; English.
XX
CC The present invention provides a human glutamate receptor delta-1 subunit
CC polypeptide. This can be used to screen for agents which modulate the
CC activity of glutamate receptor delta-1 subunit polypeptide, which may
CC then be used in the treatment of diseases such as epilepsy, brain damage,
CC neurodegenerative disorders such as Alzheimer's disease, Huntington's
CC disease and Parkinson's disease, schizophrenia, mood disorders, pain,
CC neuropathologic pain and dementias. The present sequence is a fragment of
CC the human glutamate receptor delta-1 subunit coding sequence
XX
SQ Sequence 156 BP; 41 A; 45 C; 44 G; 26 T; 0 U; 0 Other;
Query Match 17.3%; Score 26.6; DB 6; Length 156;
Best Local Similarity 60.3%; Pred. No. 2e+03;
Matches 44; Conservative 0; Mismatches 29; Indels 0; Gaps 0;
QY 23 TCATCGTCGAGTCGGCGCGGAGCTGTGTCATCTCGCTCATGTCGATCGCGCGGCC 82
Db 80 TCATCGTTGAGCTCAGGTCGATACCGCCCACTGGAACACCTGTCTCTTGCGCGG 21
QY 83 GACTCGACGATGA 95
Db 20 TTCTCCTCGAAGA 8
RESULT 25
AAL44706
ID AAL44706 standard; DNA; 190 BP.
XX
AC AAL44706;
XX
DT 03-MAY-2002 (first entry)
XX
DE Human glutamate receptor delta-1 subunit coding sequence SEQ ID NO: 2.
XX
KW Human; glutamate receptor delta-1 subunit; epilepsy; brain damage;
KW neurodegenerative disorder; Huntington's disease; Parkinson's disease;
KW Alzheimer's disease; schizophrenia; mood disorder; dementia;
KW neuropathological pain; pain; receptor; anticonvulsant; nootropic;
KW neuroprotective; vasotropic; analgesic; neuroleptic; cytostatic;
KW uropathic; antiparkinsonian; vulnerary; gene; ds.
XX
OS Homo sapiens.
XX
PN WO200206313-A2.
XX
PD 24-JAN-2002.
XX
PF 13-JUL-2001; 2001WO-EP008102.
XX
PR 18-JUL-2000; 2000US-0218835P.
XX
PA (FARB) BAYER AG.
XX
PI Kossida S;
XX
DR WPI; 2002-195800/25.

XX Novel human glutamate receptor delta-1 subunit protein which can be
PT regulated for treating epilepsy, schizophrenia, neurodegenerative
PT diseases, ischemia, pain, benign prostate hyperplasia and urinary
PT incontinence.
XX
PS Disclosure; Fig 2; 97pp; English.
XX
CC The present invention provides a human glutamate receptor delta-1 subunit
CC polypeptide. This can be used to screen for agents which modulate the
CC activity of glutamate receptor delta-1 subunit polypeptide, which may
CC then be used in the treatment of diseases such as epilepsy, brain damage,
CC neurodegenerative disorders such as Alzheimer's disease, Huntington's
CC disease and Parkinson's disease, schizophrenia, mood disorders, pain,
CC neuropathologic pain and dementias. The present sequence is a fragment of
CC the human glutamate receptor delta-1 subunit coding sequence
XX
SQ Sequence 190 BP; 45 A; 57 C; 53 G; 35 T; 0 U; 0 Other;

Query Match 17.3%; Score 26.6; DB 6; Length 190;
Best Local Similarity 60.3%; Pred. No. 2e+03;
Matches 44; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 60 TCATCGTCAGTCGGCGCCGCGACTGCAGCATGAGCGAGATGACCAGTCCGCGCC 119
DB 20 TCTTCGAGGAGAACGCGCGCCAGGACGACAGGAGGTGTTCCAGTTGGCGGTATCCGACTGA 79

QY 120 GACTCGACGATGA 132
DB 80 GCCTCAACGATGA 92

RESULT 26
AAL44706/C
ID AAL44706 standard; DNA; 190 BP.
XX
AC AAL44706;
XX
DT 03-MAY-2002 (first entry)
XX
DE Human glutamate receptor delta-1 subunit coding sequence SEQ ID NO: 2.
XX
KW Human; glutamate receptor delta-1 subunit; epilepsy; brain damage;
KW neurodegenerative disorder; Huntington's disease; Parkinson's disease;
KW Alzheimer's disease; schizophrenia; mood disorder; dementia;
KW neuropathologic pain; pain; receptor; anticonvulsant; nootropic;
KW neuroprotective; vasotropic; analgesic; neuroleptic; cyostatic;
KW uropathic; antiparkinsonian; vulnerary; gene; ds.
XX
OS Homo sapiens.
XX
PN WO200206313-A2.
XX
PD 24-JAN-2002.
XX
PF 13-JUL-2001; 2001WO-EP008102.
XX
PR 18-JUL-2000; 2000US-021835P.
XX
PA (FARB) BAYER AG.
XX
PI Kossida S;
XX
DR WPI; 2002-195800/25.
XX
PT Novel human glutamate receptor delta-1 subunit protein which can be
PT regulated for treating epilepsy, schizophrenia, neurodegenerative
PT diseases, ischemia, pain, benign prostate hyperplasia and urinary
PT incontinence.
XX
PS Disclosure; Fig 2; 97pp; English.
XX
CC The present invention provides a human glutamate receptor delta-1 subunit

CC polypeptide. This can be used to screen for agents which modulate the
CC activity of glutamate receptor delta-1 subunit polypeptide, which may
CC then be used in the treatment of diseases such as epilepsy, brain damage,
CC neurodegenerative disorders such as Alzheimer's disease, Huntington's
CC disease and Parkinson's disease, schizophrenia, mood disorders, pain,
CC neuropathologic pain and dementias. The present sequence is a fragment of
CC the human glutamate receptor delta-1 subunit coding sequence
XX
SQ Sequence 190 BP; 45 A; 57 C; 53 G; 35 T; 0 U; 0 Other;

Query Match 17.3%; Score 26.6; DB 6; Length 190;
Best Local Similarity 60.3%; Pred. No. 2e+03;
Matches 44; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 23 TCATCGTCAGTCGGCGCCGAGCTGTGTCATCTGCTCATGTCGAGTCGCGCGCCGCC 82
DB 92 TCATCGTTGAGGCTCAGGTCGATACCGCCAACTGGAACCCCTGTCCTTGGCCGCG 33

QY 83 GACTCGACGATGA 95
DB 32 TTCTCCTCGAAGA 20

RESULT 27
AAC09904
ID AAC09904 standard; cDNA; 195 BP.
XX
AC AAC09904;
XX
DT 06-OCT-2000 (first entry)
XX
DE Human secreted protein 5' EST, SEQ ID NO: 13979.
XX
KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KW gene therapy; chromosome mapping; ss.
XX
OS Homo sapiens.
XX
PN EP1033401-A2.
XX
PD 06-SEP-2000.
XX
PF 21-FEB-2000; 2000EP-00200610.
XX
PR 26-FEB-1999; 99US-0122487P.
XX
PA (GEST) GENSET.
XX
PI Dumas Milne Edwards J, Duclert A, Giordano J;
XX
DR WPI; 2000-500381/45.
XX
PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for
PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
PT diagnostic, forensic, gene therapy and chromosome mapping procedures.
XX
PS Claim 1; SEQ ID NO 13979; 71pp + Sequence Listing; English.
XX
CC The present sequence is one of a large number of 5' ESTs derived from
CC mRNAs encoding secreted proteins. No ORF has yet been conclusively
CC identified within the present sequence. The 5' ESTs were prepared from
CC total human RNAs or polyA+ RNAs derived from 30 different tissues. EST
CC sequences usually correspond mainly to the 3' untranslated region (UTR)
CC of the mRNA because they are often obtained from oligo-dT primed cDNA
CC libraries. Such ESTs are not well suited for isolating cDNA sequences
CC derived from the 5' ends of mRNAs and even in those cases where longer
CC cDNA sequences have been obtained, the full 5' UTR is rarely included. 5'
CC ESTs are derived from mRNAs with intact 5' ends and can therefore be used
CC to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in
CC diagnostic, forensic, gene therapy and chromosome mapping procedures.
CC They are used to obtain upstream regulatory sequences and to design
CC expression and secretion vectors
XX

SO Sequence 195 BP; 23 A; 79 C; 58 G; 32 T; 0 U; 3 Other;

Query Match 17.3%; Score 26.6; DB 3; Length 195;
Best Local Similarity 56.2%; Pred. No. 2e+03;
Matches 50; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

QY 37 GCGGCCGAGCTGTCATCTCGTCATCGTCGAGTCGGCGCGCCGACTCGACGATGAG 96
DB 46 GCTGCGCGCGCGRGTGTCTCGCTCGCGGAGTTTCTTCTCGCTCGGCTCGGCCTAGT 105
QY 97 CGAGATGACCACTCCGCGCCGCGACTCG 125
DB 106 CTACGTCCCGCAGCTCAGCCGCGGCTCG 134

RESULT 28
AAC09904/c
ID AAC09904 standard; cDNA; 195 BP.

AC AAC09904;
XX
DT 06-OCT-2000 (first entry)

DE Human secreted protein 5' EST, SEQ ID NO: 13979.

KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KW gene therapy; chromosome mapping; ss.

OS Homo sapiens.

XX
PN EP1033401-A2.

XX
PD 06-SEP-2000.

PF 21-FEB-2000; 2000EP-00200610.

XX
PR 26-FEB-1999; 99US-0122487P.

XX
PA (GEST) GENSET.

PI Dumae Milne Edwards J, Duclert A, Giordano J;

DR WPI; 2000-500381/45.

PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for
PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
PT diagnostic, forensic, gene therapy and chromosome mapping procedures.

PS Claim 1; SEQ ID NO 13979; 71pp + Sequence Listing; English.

CC The present sequence is one of a large number of 5' ESTs derived from
CC mRNAs encoding secreted proteins. No ORF has yet been conclusively
CC identified within the present sequence. The 5' ESTs were prepared from
CC total human RNAs or polyA+ RNAs derived from 30 different tissues. EST
CC sequences usually correspond mainly to the 3' untranslated region (UTR)
CC of the mRNA because they are often obtained from oligo-dT primed cDNA
CC libraries. Such ESTs are not well suited for isolating cDNA sequences
CC derived from the 5' ends of mRNAs and even in those cases where longer
CC cDNA sequences have been obtained, the full 5' UTR is rarely included. 5'
CC ESTs are derived from mRNAs with intact 5' ends and can therefore be used
CC to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in
CC diagnostic, forensic, gene therapy and chromosome mapping procedures.
CC They are used to obtain upstream regulatory sequences and to design
CC expression and secretion vectors

XX
SQ Sequence 195 BP; 23 A; 79 C; 58 G; 32 T; 0 U; 3 Other;

Query Match 17.3%; Score 26.6; DB 3; Length 195;
Best Local Similarity 56.2%; Pred. No. 2e+03;
Matches 50; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

QY 30 CGAGTCGCGCGCGAGCTGTCATCTCGTCATCGTCGAGTCGGCGCGCCGCGACTCGA 89
||||| ||||||| ||||||| | | | ||||| |||||

DB 134 CGAGCCGCGGCTGAGCTGGGAGCTAGACCTAGGCCGAGCCGAGCGAAGAAATCC 75

QY 90 CGATGACCGAGATGACCACTCCGCGCC 118
DB 74 CGCCGACGCGAGACACACGCGCCGCGCAGC 46

RESULT 29
AAL17387
ID AAL17387 standard; cDNA; 170 BP.

AC AAL17387;

DT 07-DEC-2001 (first entry)

DE Human breast cancer expressed polynucleotide 9844.

KW Human; breast cancer; cell marker; cytostatic; ss.

OS Homo sapiens.

XX
PN WO200151628-A2.

XX
PD 19-JUL-2001;

PF 10-JAN-2001; 2001WO-US000798.

XX
PR 14-JAN-2000; 2000US-0176077P.

XX
PR 14-MAR-2000; 2000US-0189167P.

XX
PR 24-MAR-2000; 2000US-0192039P.

XX
PR 29-MAR-2000; 2000US-0193480P.

XX
PR 15-MAY-2000; 2000US-0205230P.

XX
PR 09-JUN-2000; 2000US-0211315P.

XX
PR 25-JUL-2000; 2000US-0220534P.

XX
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

PI Lillie J, Xu Y, Wang Y, Steinmann K;

DR WPI; 2001-451856/48.

PT New peptide useful as a marker for the diagnosis of breast cancer.

PS Claim 1; Page 1753; 3695pp; English.

CC The invention relates to human breast cancer expressed polynucleotides
CC (AAL07544-AAL26789) and methods of assessing whether a patient is
CC afflicted with breast cancer by examining the correlation between the
CC expression of certain markers and the cancerous state of breast cells.
CC The polynucleotides and encoded polypeptides are potential markers for
CC detecting, diagnosing, monitoring, characterising treating and
CC potentially preventing breast cancer. The polynucleotides and encoded
CC polypeptides are also useful for isolating compounds with cytostatic
CC activity

XX
SQ Sequence 170 BP; 25 A; 50 C; 64 G; 31 T; 0 U; 0 Other;

Query Match 16.9%; Score 26; DB 4; Length 170;
Best Local Similarity 55.6%; Pred. No. 2.8e+03;
Matches 50; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

QY 61 CATCGTCGAGTCGCGCGCGCGCGACTCGACGATGAGCGAGATGACCACTCCGCGCGCC 120
DB 18 CTTGTCGCGCGCGGTTCTGTGTCGATGCGCGCGGTGACGATGGGGCTGCGTCCGGCGGCA 77

QY 121 ACTGACGATGACCGAGATGACCACTCCG 150
DB 78 GCTGTCGATCACCGACACTTCCAGGTCGG 107

RESULT 30
AAL17387/c
ID AAL17387 standard; cDNA; 170 BP.

XX	AAL17387;
AC	07-DEC-2001 (first entry)
DT	Human breast cancer expressed polynucleotide 9844.
DE	Human; breast cancer; cell marker; cytostatic; ss.
XX	Homo sapiens.
OS	WO200151628-A2.
PN	19-JUL-2001.
PD	10-JAN-2001; 2001WO-US000798.
PF	14-JAN-2000; 2000US-0176077P.
XX	14-MAR-2000; 2000US-0189167P.
PR	24-MAR-2000; 2000US-0192099P.
PR	29-MAR-2000; 2000US-0193480P.
PR	15-MAY-2000; 2000US-0205230P.
PR	09-JUN-2000; 2000US-0211315P.
PR	25-JUL-2000; 2000US-0220534P.
PA	(MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
PI	Lillie J, Xu Y, Wang Y, Steinmann K;
XX	WPI; 2001-451856/48..
DR	New peptide useful as a marker for the diagnosis of breast cancer.
PT	Claim 1; Page 1753; 3695pp; English.
PS	The invention relates to human breast cancer expressed polynucleotides
XX	(AAL07544-AAL26789) and methods of assessing whether a patient is
CC	afflicted with breast cancer by examining the correlation between the
CC	expression of certain markers and the cancerous state of breast cells.
CC	The polynucleotides and encoded polypeptides are potential markers for
CC	detecting, diagnosing, monitoring, characterising treating and
CC	potentially preventing breast cancer. The polynucleotides and encoded
CC	polypeptides are also useful for isolating compounds with cytostatic
CC	activity
SC	Sequence 170 BP; 25 A; 50 C; 64 G; 31 T; 0 U; 0 Other;
SQ	Query Match 16.9%; Score 26; DB 4; Length 170;
	Best Local Similarity 55.6%; Pred. No. 2.8e+03;
	Matches 50; Conservative 0; Mismatches 40; Indels 0; Gaps 0;
OY	5 CGAGCTGTGCATCTCGCTCATGTCGAGTCGGCGGCCGAAGTGTCACTCCTCATC 64
DB	107 CCGACTTGGAAGTGTGGTATCGACGAGCTGCCGCCGAGCGAGCCCCATCGTCACGC 48
OY	65 GTCGAGTCGGCGCGGCCGCCGACTCGACGATG 94
DB	47 GCCGCATCGACCAGAACCCGGCGCGCACGAAG 18
RESULT 31	
AAL09498	
ID	AAL09498 standard; cDNA; 189 BP.
AC	AAL09498;
XX	07-DEC-2001 (first entry)
DT	Human breast cancer expressed polynucleotide 1955.
DE	Human; breast cancer; cell marker; cytostatic; ss.
XX	Homo sapiens.
OS	

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XX      :
PN      WO200151628-A2.
XX
PD      19-JUL-2001.
XX
PF      10-JAN-2001; 2001WO-US000798.
XX
PR      14-JAN-2000; 2000US-0176077P.
PR      14-MAR-2000; 2000US-0189167P.
PR      24-MAR-2000; 2000US-0192099P.
PR      29-MAR-2000; 2000US-0193480P.
PR      15-MAY-2000; 2000US-0205230P.
PR      09-JUN-2000; 2000US-0211315P.
PR      25-JUL-2000; 2000US-0220534P.
XX
PA      (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
PI      Lillie J, Xu Y, Wang Y, Steinmann K;
DR      WPI; 2001-451856/48.
XX
PT      New peptide useful as a marker for the diagnosis of breast cancer.
PS      Claim 1; Page 382; 3695pp; English.
XX
XX      The invention relates to human breast cancer expressed polynucleotides
CC      (AAL07544-AAL26789) and methods of assessing whether a patient is
CC      afflicted with breast cancer by examining the correlation between the
CC      expression of certain markers and the cancerous state of breast cells.
CC      The polynucleotides and encoded polypeptides are potential markers for
CC      detecting, diagnosing, monitoring, characterising treating and
CC      potentially preventing breast cancer. The polynucleotides and encoded
CC      polypeptides are also useful for isolating compounds with cytostatic
CC      activity
XX
SQ      Sequence 189 BP; 25 A; 58 C; 74 G; 32 T; 0 U; 0 Other;
XX
Query Match          16.9%; Score 26; DB 4; Length 189;
Best/Local Similarity 55.6%; Pred. No. 2.8e+03;
Matches 50; Conservative 0; Mismatches 40; Indels 0; Gaps 0;
QY      61 CATCGTCGAGTCGCGCGCGCCGCACTCGACGATGAGCGAGATGACCAGCTCCGCGCGCCG 120
        |||||
DB      33 CTTCGTCGCGCGCGGTCTGTGTCGATGGCGCGCGTGACGATGGGGCTGCGTCCGCGCGCA 92
QY      121 ACTCGACGATGAGCGAGATGACCACTCCG 150
        |||||
DB      93 GCTCGTCGATCACCGACACTTCCAGGTCGG 122
XX
RESULT 32
AAL09498/c
ID      AAL09498 standard; cDNA; 189 BP.
XX
XX      AAL09498;
AC
XX      07-DEC-2001 (first entry)
DT
XX
DE      Human breast cancer expressed polynucleotide 1955.
XX
KW      Human; breast cancer; cell marker; cytostatic; ss.
XX
OS      Homo sapiens.
XX
PN      WO200151628-A2.
XX
PD      19-JUL-2001.
XX
PF      10-JAN-2001; 2001WO-US000798.
XX
PR      14-JAN-2000; 2000US-0176077P.
PR      14-MAR-2000; 2000US-0189167P.
PR      24-MAR-2000; 2000US-0192099P.
PR      29-MAR-2000; 2000US-0193480P.
PR      15-MAY-2000; 2000US-0205230P.
PR      09-JUN-2000; 2000US-0211315P.
PR      25-JUL-2000; 2000US-0220534P.
XX

```


PR 29-MAR-2000; 2000US-0193480P.
 PR 15-MAY-2000; 2000US-0205230P.
 PR 09-JUN-2000; 2000US-0211315P.
 PR 25-JUL-2000; 2000US-0220534P.
 XX
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 XX
 PI Lillie J, Xu Y, Wang Y, Steinmann K;
 XX
 DR WPI; 2001-451856/48.
 XX
 PT New peptide useful as a marker for the diagnosis of breast cancer.
 XX
 PS Claim 1; Page 382; 3695pp; English.
 XX
 CC The invention relates to human breast cancer expressed polynucleotides
 CC (AAL07544-AAL26789) and methods of assessing whether a patient is
 CC afflicted with breast cancer by examining the correlation between the
 CC expression of certain markers and the cancerous state of breast cells.
 CC The polynucleotides and encoded polypeptides are potential markers for
 CC detecting, diagnosing, monitoring, characterising treating and
 CC potentially preventing breast cancer. The polynucleotides and encoded
 CC polypeptides are also useful for isolating compounds with cytostatic
 CC activity
 XX
 SQ Sequence 189 BP; 25 A; 58 C; 74 G; 32 T; 0 U; 0 Other;
 Query Match 16.9%; Score 26; DB 4; Length 189;
 Best Local Similarity 55.6%; Pred. No. 2.8e+03;
 Matches 50; Conservative 0; Mismatches 40; Indels 0; Gaps 0;
 OY 5 CGGAGCTGTCATCTCGCTCATCTGTCGAGTCGGCGCGGAGCTGTCATCTCGCTCATC 64
 Db 122 CCGACCTGGAAGTGTGCTGATGACGAGCTGCCGCCGAGCAGCCCCCATCTGCACGC 63
 OY 65 GTCGAGTCGGCGCGCGCGCGGACTCGACGATG 94
 Db 62 GCGCCATCGACCAAGAACCGCGCGCAGCAAG 33
 RESULT 33
 AAT49353
 ID AAT49353 standard; DNA; 183 BP.
 XX
 AC AAT49353;
 XX
 DT 10-SEP-1997 (first entry)
 XX
 DE N. fischeri internal transcribed spacer 1 sequence.
 XX
 KW Filamentous; fungus; Byssoschlamys nivea; Neosartorya fischeri; primer;
 KW Zygosaccharomyces bailii; PCR; amplification; polymerase chain reaction;
 KW ribosomal internal spacer; detection; heat resistant; fruit;
 KW microorganism; contaminant; strawberry; foodstuff; ss.
 XX
 OS Neosartorya fischeri.
 XX
 PN WO9638587-A2.
 XX
 PD 05-DEC-1996.
 XX
 PF 31-MAY-1996; 96WO-FR000821.
 XX
 PR 02-JUN-1995; 95FR-00006578.
 XX
 PA (UNIR-) UNIR ULTRA PROPRE NUTRITION IND RECH.
 XX
 PI Chravavez E, Aufrere R;
 XX
 DR WPI; 1997-034393/03.
 XX
 PT Primers derived from internal transcribed spacer sequences - used to
 PT detect contaminants of foodstuffs, esp Byssoschlamys nivea, Neosartorya

PT fischeri or Zygosaccharomyces bailii.
 XX
 PS Claim 1; Page 12; 18pp; French.
 XX
 CC The invention relates to methods to detect the filamentous fungi
 CC Byssoschlamys nivea, Neosartorya fischeri and Zygosaccharomyces bailii by
 CC PCR amplification on genomic DNA using primers derived from the ribosomal
 CC internal transcribed spacer (ITS) sequences (see AAT49351-6). This
 CC sequence represents the ITS1 from N. neosartorya and is amplified by the
 CC primers AAT49359-60. The method is used to detect heat resistant
 CC microorganisms of the above species which are important contaminants of
 CC fruit, especially strawberry-based foodstuffs
 XX
 SQ Sequence 183 BP; 30 A; 62 C; 52 G; 39 T; 0 U; 0 Other;
 Query Match 16.6%; Score 25.6; DB 2; Length 183;
 Best Local Similarity 59.7%; Pred. No. 3.5e+03;
 Matches 43; Conservative 0; Mismatches 29; Indels 0; Gaps 0;
 OY 64 CGTCGAGTCGGCGCGCGCGGACTCGACGATGAGGAGATGACCAAGCTCCGCGCGGACT 123
 Db 67 CGCCGTTTCGACGCGCGCGCGGAGAGGCTCGCGCCCCCGCGCGCGCGGAGAGCC 126
 OY 124 CGACGATGACCG 135
 Db 127 CCAACATGAACG 138

RESULT 34
 AAT49353/c
 ID AAT49353 standard; DNA; 183 BP.
 XX
 AC AAT49353;
 XX
 DT 10-SEP-1997 (first entry)
 XX
 DE N. fischeri internal transcribed spacer 1 sequence.
 XX
 KW Filamentous; fungus; Byssoschlamys nivea; Neosartorya fischeri; primer;
 KW Zygosaccharomyces bailii; PCR; amplification; polymerase chain reaction;
 KW ribosomal internal transcribed spacer; detection; heat resistant; fruit;
 KW microorganism; contaminant; strawberry; foodstuff; ss.
 XX
 OS Neosartorya fischeri.
 XX
 PN WO9638587-A2.
 XX
 PD 05-DEC-1996.
 XX
 PF 31-MAY-1996; 96WO-FR000821.
 XX
 PR 02-JUN-1995; 95FR-00006578.
 XX
 PA (UNIR-) UNIR ULTRA PROPRE NUTRITION IND RECH.
 XX
 PI Chravavez E, Aufrere R;
 XX
 DR WPI; 1997-034393/03.
 XX
 PT Primers derived from internal transcribed spacer sequences - used to
 PT detect contaminants of foodstuffs, esp Byssoschlamys nivea, Neosartorya
 PT fischeri or Zygosaccharomyces bailii.
 XX
 PS Claim 1; Page 12; 18pp; French.
 XX
 CC The invention relates to methods to detect the filamentous fungi
 CC Byssoschlamys nivea, Neosartorya fischeri and Zygosaccharomyces bailii by
 CC PCR amplification on genomic DNA using primers derived from the ribosomal
 CC internal transcribed spacer (ITS) sequences (see AAT49351-6). This
 CC sequence represents the ITS1 from N. neosartorya and is amplified by the
 CC primers AAT49359-60. The method is used to detect heat resistant
 CC microorganisms of the above species which are important contaminants of
 CC fruit, especially strawberry-based foodstuffs

XX Sequence 183 BP; 30 A; 62 C; 52 G; 39 T; 0 U; 0 Other;
SQ Query Match 16.6%; Score 25.6; DB 2; Length 183;
Best Local Similarity 59.7%; Pred. No. 3.5e+03;
Matches 43; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 20 CGCTCATCGTCGAGTCGGCGCGGAGCTGTGCATCTGCTCATCTGAGTCGGCGCC 79
DB 138 CGTTCATGTTGGGCTTTCGGCGGGCGCGGCGCGGCGGAGGCTCCCGCGCGCC 79

QY 80 GCCGACTCGACG 91
DB 78 GTCGAACGCGC 67

RESULT 35
AAA94339
ID AAA94339 standard; DNA; 123 BP.
XX AAA94339;
AC
XX 11-JAN-2001 (first entry)
DT
XX 123-mer DNA PP.01.
DE
XX RNA-protein fusion; protein library; protein isolation; gene cloning; ss.
KM
XX Synthetic.
OS
XX WO200047775-A1.
PN
XX 17-AUG-2000.
PD
XX 01-FEB-2000; 2000WO-US002589.
PF
XX 09-FEB-1999; 99US-00247190.
PR
XX (GEHO) GEN HOSPITAL CORP.
PA
XX Szostak JW, Roberts RW, Liu R;
PI
XX WPI; 2000-533022/48.
DR
XX
XX Producing protein or DNA libraries which are useful for improving
PT existing proteins, by in vitro translating protein coding sequences to
PT produce RNA-protein fusions and incubating these protein fusions under
PT high salt conditions.
PT
XX Disclosure; Page 72; 121pp; English.
PS
XX The present sequence was used in a method for generating RNA-protein
CC fusions, which comprise a protein covalently linked to the 3' end of its
CC own mRNA. The fusions are made by synthesis and in vitro or in situ
CC translation of an mRNA molecule with a peptide acceptor attached to its
CC 3' end. The RNA-protein fusions are incubated under high salt conditions
CC to produce a protein library. This method is useful for improving or
CC altering existing proteins, as well as for isolating new proteins and
CC nucleic acid or small molecule targets. It may also be used to improve
CC human or humanised single-chain antibodies for the treatment of a number
CC of diseases. The method is useful for the isolation of proteins with
CC specific binding properties, for screening cDNA libraries and cloning new
CC genes on the basis of protein-protein interactions. Unlike prior art, the
CC new method does not rely on maintaining the integrity of an
CC mRNA:ribosome:nascent chain ternary complex, which is very fragile and is
CC therefore of limited use. The method does not rely on topological links
CC between the protein and the nucleic acid so that the information of the
CC protein is retained and can be recovered in readable, nucleic acid form
CC
XX Sequence 123 BP; 4 A; 15 C; 8 G; 15 T; 0 U; 81 Other;
SQ Query Match 16.2%; Score 25; DB 3; Length 123;
Best Local Similarity 15.0%; Pred. No. 4.8e+03;

Matches 16; Conservative 26; Mismatches 65; Indels 0; Gaps 0;

QY 18 CTCGTCATCGTCGAGTCGGCGCGGAGCTGTGCATCTGCTCATCTGAGTCGGCGG 77
DB 12 CTTGTGCATCSNNSNNSNNSNNSNNSNNSNNSNNSNNSNNSNNSNNSN 71

QY 78 CCGCCGACTCGACGATGAGCGAGATGACACGCTCCGCGCGGACTC 124
DB 72 NSNNSNNSNNSNNSNNSNNSNNSNNSNNSNNSNNSNNSNCTCCTCGCCCTTGCTC 118

RESULT 36
AAA94339/C
ID AAA94339 standard; DNA; 123 BP.
XX AAA94339;
AC
XX 11-JAN-2001 (first entry)
DT
XX 123-mer DNA PP.01.
DE
XX RNA-protein fusion; protein library; protein isolation; gene cloning; ss.
KM
XX Synthetic.
OS
XX WO200047775-A1.
PN
XX 17-AUG-2000.
PD
XX 01-FEB-2000; 2000WO-US002589.
PF
XX 09-FEB-1999; 99US-00247190.
PR
XX (GEHO) GEN HOSPITAL CORP.
PA
XX Szostak JW, Roberts RW, Liu R;
PI
XX WPI; 2000-533022/48.
DR
XX
XX Producing protein or DNA libraries which are useful for improving
PT existing proteins, by in vitro translating protein coding sequences to
PT produce RNA-protein fusions and incubating these protein fusions under
PT high salt conditions.
PT
XX Disclosure; Page 72; 121pp; English.
PS
XX The present sequence was used in a method for generating RNA-protein
CC fusions, which comprise a protein covalently linked to the 3' end of its
CC own mRNA. The fusions are made by synthesis and in vitro or in situ
CC translation of an mRNA molecule with a peptide acceptor attached to its
CC 3' end. The RNA-protein fusions are incubated under high salt conditions
CC to produce a protein library. This method is useful for improving or
CC altering existing proteins, as well as for isolating new proteins and
CC nucleic acid or small molecule targets. It may also be used to improve
CC human or humanised single-chain antibodies for the treatment of a number
CC of diseases. The method is useful for the isolation of proteins with
CC specific binding properties, for screening cDNA libraries and cloning new
CC genes on the basis of protein-protein interactions. Unlike prior art, the
CC new method does not rely on maintaining the integrity of an
CC mRNA:ribosome:nascent chain ternary complex, which is very fragile and is
CC therefore of limited use. The method does not rely on topological links
CC between the protein and the nucleic acid so that the information of the
CC protein is retained and can be recovered in readable, nucleic acid form
CC
XX Sequence 123 BP; 4 A; 15 C; 8 G; 15 T; 0 U; 81 Other;
SQ Query Match 16.2%; Score 25; DB 3; Length 123;
Best Local Similarity 15.0%; Pred. No. 4.8e+03;
Matches 16; Conservative 26; Mismatches 65; Indels 0; Gaps 0;

QY 31 GAGTCGGCGCGGAGCTGTGCATCTGCTCATCTGAGTCGGCGCGGAGCTGAC 90
DB 118 GAGCAAGGCGGAGGAGNNSNNSNNSNNSNNSNNSNNSNNSNNSNNSNNSN 59

QY 91 GATGAGCGAGATGACCACTCCGCCCGCGACTCGACGATGAGCGAG 137
Db 58 SNNNSNNNSNNNSNNNSNNNSNNNSNNNSNNNSNNSGATGACACAAG 12

RESULT 37

ACH88658 ID ACH88658 standard; DNA; 108 BP.
AC ACH88658;
DT 29-JUL-2004 (first entry)
DE Human genome derived single exon probe #21853.
XX Human; probe; ss; gene expression; single exon probe; microarray;
KW alternative splicing event; genomic alteration.
XX Homo sapiens.
OS
XX US2003194704-A1.
PN
XX 16-OCT-2003.
PD
XX 03-APR-2002; 2002US-00029386.
PF
XX 03-APR-2002; 2002US-00029386.
PR
XX (PENN/) PENN S G.
PA (RANK/) RANK D R.
PA (HANZ/) HANZEL D K.
XX
PI Penn SG, Rank DR, Hanzel DK;
XX WPI; 2004-119264/12.

PT New human genome-derived single exon nucleic acid probes useful for human
PT gene expression analysis, for identifying or characterizing alternative
PT splicing events, for assessing genomic alterations or as tools for
PT surveying tissues.

PS Claim 1; SEQ ID NO 21853; 80pp; English.

XX The invention relates to a nucleic acid probe for measuring human gene
CC expression, comprising any of the 27,400 fully defined nucleotide
CC sequences in the specification, or their complements or fragments, and
CC encoding at least 8 amino acids of any of the 6888 amino acid sequences
CC fully defined in the specification. The probe is a single exon probe that
CC hybridises under high stringency conditions to a nucleic acid molecule
CC expressed in human cells or tissues. Also included are a spatially-
CC addressable set of single exon nucleic acid probes for measuring human
CC gene expression (comprising a plurality of single exon nucleic acid
CC probes cited above, where each of the plurality of probes is separately
CC and addressably isolatable or amplifiable from the plurality), a single
CC exon microarray for measuring human gene expression, a method of
CC measuring human gene expression, a vector comprising the single exon
CC probe cited above, an ORF-encoded peptide comprising at least 8
CC contiguous amino acids of any of the above-mentioned amino acid
CC sequences (optionally with conservative amino acid substitutions), an
CC isolated antibody that binds specifically to a peptide cited above,
CC methods of selling and/or licensing single exon probes or microarrays to
CC a customer desiring to measure gene expression, a method of providing
CC human gene expression data by subscription, and a computer-readable
CC storage medium which contains a database having a plurality of records
CC (each record including data on the expression of a single exon probe
CC cited above. The probe, methods and apparatus are useful in gene
CC expression analysis. The probes may be used as tools for surveying
CC tissues to detect the presence of expressed messages that contain their
CC specific exon, or in constructing genome-derived single exon microarrays.
CC In addition, the probes are used in identifying and characterising
CC alternative splicing events, in detecting and characterising gross
CC alterations in the genomic locus that includes their exon, in assessing

CC smaller genomic alterations, in priming the synthesis of nucleic acids,
CC or in expressing the ORF-encoded peptide. The present sequence is a human
CC single exon probe of the invention. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?DocId=20030194704

XX Sequence 108 BP; 15 A; 39 C; 34 G; 20 T; 0 U; 0 Other;

SO Query: Match 16.1%; Score 24.8; DB 12; Length 108;
Best local Similarity 72.7%; Pred. No. 5.3e+03;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 106 CAGCTCCGCCCGCGACTCGACGATGAGCGAGATGACCACTCC 149
Db 5 CTGCTCTGCGCCGCCCTCGCTCGAGCCGGAGACCACTTC 48

RESULT 38

ACH88658/c ID ACH88658 standard; DNA; 108 BP.
XX
AC ACH88658;
XX
DT 29-JUL-2004 (first entry)
DE Human genome derived single exon probe #21853.
XX
DE Human; probe; ss; gene expression; single exon probe; microarray;
KW alternative splicing event; genomic alteration.
XX
OS Homo sapiens.
XX
PN US2003194704-A1.
XX
PD 16-OCT-2003.
XX
PF 03-APR-2002; 2002US-00029386.
XX
XX 03-APR-2002; 2002US-00029386.
PR
XX (PENN/) PENN S G.
PA (RANK/) RANK D R.
PA (HANZ/) HANZEL D K.
XX
PI Penn SG, Rank DR, Hanzel DK;
XX WPI; 2004-119264/12.

DR
XX
PT New human genome-derived single exon nucleic acid probes useful for human
PT gene expression analysis, for identifying or characterizing alternative
PT splicing events, for assessing genomic alterations or as tools for
PT surveying tissues.

PS Claim 1; SEQ ID NO 21853; 80pp; English.

XX The invention relates to a nucleic acid probe for measuring human gene
CC expression, comprising any of the 27,400 fully defined nucleotide
CC sequences in the specification, or their complements or fragments, and
CC encoding at least 8 amino acids of any of the 6888 amino acid sequences
CC fully defined in the specification. The probe is a single exon probe that
CC hybridises under high stringency conditions to a nucleic acid molecule
CC expressed in human cells or tissues. Also included are a spatially-
CC addressable set of single exon nucleic acid probes for measuring human
CC gene expression (comprising a plurality of single exon nucleic acid
CC probes cited above, where each of the plurality of probes is separately
CC and addressably isolatable or amplifiable from the plurality), a single
CC exon microarray for measuring human gene expression, a method of
CC measuring human gene expression, a vector comprising the single exon
CC probe cited above, an ORF-encoded peptide comprising at least 8
CC contiguous amino acids of any of the above-mentioned amino acid
CC sequences (optionally with conservative amino acid substitutions), an
CC isolated antibody that binds specifically to a peptide cited above,

CC methods of selling and/or licensing single exon probes or microarrays to
CC a customer desiring to measure gene expression, a method of providing
CC human gene expression data by subscription, and a computer-readable
CC storage medium which contains a database having a plurality of records
CC (each record including data on the expression of a single exon probe
CC cited above. The probe, methods and apparatus are useful in gene
CC expression analysis. The probes may be used as tools for surveying
CC tissues to detect the presence of expressed messages that contain their
CC specific exon, or in constructing genome-derived single exon microarrays.
CC In addition, the probes are used in identifying and characterizing
CC alternative splicing events, in detecting and characterizing gross
CC alterations in the genomic locus that includes their exon, in assessing
CC smaller genomic alterations, in priming the synthesis of nucleic acids,
CC or in expressing the ORF-encoded peptide. The present sequence is a human
CC single exon probe of the invention. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?DocID=20030194704
XX
SQ Sequence 108 BP; 15 A; 39 C; 34 G; 20 T; 0 U; 0 Other;

Query Match 16.1%; Score 24.8; DB 12; Length 108;
Best Local Similarity 72.7%; Pred. No. 5.3e+03;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 6 GGAGCTGTCATCTCGCTCATCTGCTGCGGCGCGGCGAGCTG 49
| | | | | | | | | | | | | | | | | | | | | |
Db 48 GAAGCTGTCCTCCGCTCCGAGCGGCGGCGGCGGCGAGCAG 5

RESULT 39
ACD96616
ID ACD96616 standard; cDNA; 130 BP.
XX
AC ACD96616;
XX
DT 23-SEP-2003 (first entry)
XX
DE Human colon cancer cell expressed cDNA #5028.
XX
XX Open reading frame detection; genome sequencing; colon cancer;
KW breast cancer; population genome analysis; genetic shift; cancer;
KW antibiotic resistance; antibiotic non-tolerance; congenital disease;
KW agriculture; food crop genome; resistance gene; retrovirus;
KW influenza virus; eukaryotic pathogen detection; trypanosome; Plasmodium;
KW gene; ss.
XX
XX Homo sapiens.
OS
XX
PN US2002155438-A1.
XX
PD 24-OCT-2002.
XX
PF 27-SEP-1999; 99US-00406117.
XX
PR 20-NOV-1998; 98US-00196716.
XX
PA (SIMP/) SIMPSON A J G.
PA (NETO/) NETO E D.
PA (BREN/) BRENTANI R R.
XX
PI Simpson AJG, Neto ED, Brentani RR;
XX
DR WPI; 2003-182626/18.
XX
XX
PT Determining open reading frames of genome of an organism e.g. a human
PT suffering from cancer involves use of single oligonucleotide primer at
PT low stringency for preparing single-stranded cDNA from mRNA of
PT individual.
XX
XX Example 9; Page 721; 959pp; English.
PS
XX The invention describes a method of determining open reading frames in

CC the genome of organism, comprising contacting mRNA from cell of organism
CC with a single oligonucleotide primer (I) at low stringency, preparing
CC single-stranded cDNA by reverse transcribing mRNA with (I), amplifying
CC cDNA, sequencing the product, and repeating the contacting, preparing
CC and amplifying steps with different primers and sequencing resulting
CC nucleic acids. The method is useful for: determining that a known
CC nucleotide sequence from a genome of an organism corresponds to a
CC nucleotide sequence of an open reading frame; for preparing a contig,
CC nucleic acid molecule from a genome of an organism; and for sequencing
CC all or part of a genome of an organism. mRNA is obtained from mammalian
CC or human cell which is associated with a pathological condition e.g. a
CC colon cancer or breast cancer cell. The method is useful for analyses of
CC populations of subjects and can be used to carry out genetic analyses of
CC large or small populations. further, it can be used to study living
CC systems to determine if, e.g. there have been genetic shifts which render
CC an individual or population more or less likely to be afflicted with
CC diseases such as cancer, to determine antibiotic resistance or non-
CC tolerance, and so forth. The method can also be used in the study of
CC congenital diseases, and the risk of affliction to a foetus, as well as
CC the study of whether the conditions are likely to be passed to offspring
CC through ova or sperm. The analyses for pathological conditions can be
CC carried out in all animals, plants, birds, fish, etc. Using this method,
CC in the area of agriculture, for example the genomes of food crops can be
CC studied to determine if resistance genes are present, defects in plant
CC genomes can also be studied in this way. Similarly, the method permits
CC determination of the pathogens which integrate into the genome, such as
CC retroviruses and other integrating viruses such as influenza virus, have
CC undergone shifts or mutations, which may require different approaches to
CC therapy. This method is also applied to eukaryotic pathogens, such as
CC trypanosomes, different types of Plasmodium, etc. The method essentially
CC eliminates sequencing of non-coding portions. This sequence represents a
CC polynucleotide isolated from human colon cancer cell cDNA library
XX
SQ Sequence 130 BP; 28 A; 44 C; 35 G; 23 T; 0 U; 0 Other;

Query Match 16.1%; Score 24.8; DB 10; Length 130;
Best Local Similarity 57.9%; Pred. No. 5.4e+03;
Matches 44; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 71 TCGGCGGCGCGGCTGACGATGAGCGAGATGACCACTCCGGCGGCGGACTGACGAT 130
| | | | | | | | | | | | | | | | | | | | | |
Db 26 TGGGCGAAGGAGAGGCTAACATGACGATCGACCGACTTGACCGCTGACCTGACCAT 85

QY 131 GAGCGAGATGACCGAGC 146
| | | | | | | | | | | | | | | | | | | | | |
Db 86 CTTGAGCTGACCTGC 101

RESULT 40
ACD96616/c
ID ACD96616 standard; cDNA; 130 BP.
XX
AC ACD96616;
XX
DT 23-SEP-2003 (first entry)
XX
DE Human colon cancer cell expressed cDNA #5028.
XX
XX Open reading frame detection; genome sequencing; colon cancer;
KW breast cancer; population genome analysis; genetic shift; cancer;
KW antibiotic resistance; antibiotic non-tolerance; congenital disease;
KW agriculture; food crop genome; resistance gene; retrovirus;
KW influenza virus; eukaryotic pathogen detection; trypanosome; Plasmodium;
KW gene; ss.
XX
XX Homo sapiens.
OS
XX
PN US2002155438-A1.
XX
PD 24-OCT-2002.
XX
PF 27-SEP-1999; 99US-00406117.
XX

PR 20-NOV-1998; 98US-00196716.
XX
PA (SIMP/) SIMPSON A J G.
PA (NETO/) NETO E D.
PA (BREN/) BRENTANI R R.
XX
PI Simpson AJG, Neto ED, Brentani RR;
XX
DR WPI; 2003-182626/18.
XX
PT Determining open reading frames of genome of an organism e.g. a human
PT suffering from cancer involves use of single oligonucleotide primer at
PT low stringency for preparing single-stranded cDNA from mRNA of
PT individual.
XX
PS Example 9; Page 721; 959pp; English.
XX
CC The invention describes a method of determining open reading frames in
CC the genome of organism, comprising contacting mRNA from cell of organism
CC with a single oligonucleotide primer (I) at low stringency, preparing
CC single-stranded cDNA by reverse transcribing mRNA with (I), amplifying
CC cDNA, sequencing the product, and repeating the contacting, preparing
CC and amplifying steps with different primers and sequencing resulting
CC nucleic acids. The method is useful for: determining that a known
CC nucleotide sequence from a genome of an organism corresponds to a
CC nucleotide sequence of an open reading frame; for preparing a contig,
CC nucleic acid molecule from a genome of an organism; and for sequencing
CC all or part of a genome of an organism. mRNA is obtained from mammalian
CC or human cell which is associated with a pathological condition e.g. a
CC colon cancer or breast cancer cell. The method is useful for analyses of
CC populations of subjects and can be used to carry out genetic analyses of
CC large or small populations. further, it can be used to study living
CC systems to determine if, e.g. there have been genetic shifts which render
CC an individual or population more or less likely to be afflicted with
CC diseases such as cancer, to determine antibiotic resistance or non-
CC tolerance, and so forth. The method can also be used in the study of
CC congenital diseases, and the risk of affliction to a foetus, as well as
CC the study of whether the conditions are likely to be passed to offspring
CC through ova or sperm. The analyses for pathological conditions can be
CC carried out in all animals, plants, birds, fish, etc. Using this method,
CC in the area of agriculture, for example the genomes of food crops can be
CC studied to determine if resistance genes are present, defects in plant
CC genomes can also be studied in this way. Similarly, the method permits
CC determination of the pathogens which integrate into the genome, such as
CC retroviruses and other integrating viruses such as influenza virus, have
CC undergone shifts or mutations, which may require different approaches to
CC therapy. This method is also applied to eukaryotic pathogens, such as
CC trypanosomes, different types of Plasmodium, etc. The method essentially
CC eliminates sequencing of non-coding portions. This sequence represents a
CC polynucleotide isolated from human colon cancer cell cDNA library
XX
SQ Sequence 130 BP; 28 A; 44 C; 35 G; 23 T; 0 U; 0 Other;
XX
Query Match 16.1%; Score 24.8; DB 10; Length 130;
Best Local Similarity 57.9%; Pred. No. 5.4e+03;
Matches 44; Conservative 0; Mismatches 32; Indels 0; Gaps 0;
QY 9 GCTGTCATCTCGCTCATCTGAGTGGCGCGGAGCTGTCATCTCGTCATCTGCG 68
DB 101 GCAGTCACTCAAGATGTGTGAGTCAAGCGTCAAGGTCCGATCCGATCATGTTAG 42
QY 69 AGTCGGCGCGCGCGA 84
DB 41 CCTCTGCCTTCGCCCA 26
XX
RESULT 41
AAC12537
ID AAC12537 standard; cDNA; 181 BP.
XX
AC AAC12537;
XX
DT 06-OCT-2000 (first entry)
XX

XX
DE Human secreted protein 5' EST, SEQ ID NO: 16612.
XX
KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KW gene therapy; chromosome mapping; ss.
XX
OS Homo sapiens.
XX
PN EP1033401-A2.
XX
PD 06-SEP-2000.
XX
PF 21-FEB-2000; 2000EP-00200610.
XX
PR 26-FEB-1999; 99US-0122487P..
XX
PA (GEST) GENSET.
XX
PI Dumas Milne Edwards J, Duclert A, Giordano J;
XX
DR WPI; 2000-500381/45.
XX
PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for
PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
PT diagnostic, forensic, gene therapy and chromosome mapping procedures.
XX
PS Claim 1; SEQ ID NO 16612; 71pp + Sequence Listing; English.
XX
CC The present sequence is one of a large number of 5' ESTs derived from
CC mRNAs encoding secreted proteins. No ORF has yet been conclusively
CC identified within the present sequence. The 5' ESTs were prepared from
CC total human RNAs or polyA+ RNAs derived from 30 different tissues. EST
CC sequences usually correspond mainly to the 3' untranslated region (UTR)
CC of the mRNA because they are often obtained from oligo-dT primed cDNA
CC libraries. Such ESTs are not well suited for isolating cDNA sequences
CC derived from the 5' ends of mRNAs and even in those cases where longer
CC cDNA sequences have been obtained, the full 5' UTR is rarely included. 5'
CC ESTs are derived from mRNAs with intact 5' ends and can therefore be used
CC to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in
CC diagnostic, forensic, gene therapy and chromosome mapping procedures.
CC They are used to obtain upstream regulatory sequences and to design
CC expression and secretion vectors
XX
SQ Sequence 181 BP; 35 A; 35 C; 92 G; 19 T; 0 U; 0 Other;
XX
Query Match 16.1%; Score 24.8; DB 3; Length 181;
Best Local Similarity 67.3%; Pred. No. 5.4e+03;
Matches 35; Conservative 0; Mismatches 17; Indels 0; Gaps 0;
QY 25 ATGCTGAGTGGCGGCGGAGCTGTCATCTGCTCATCTGAGTCGGCG 76
DB 20 ATCCCTACTCTGCGGGGCGCGGAGGCGTCTGCTCTTCGCGGCGGCGG 71
XX
RESULT 42
AAC12537/C
ID AAC12537 standard; cDNA; 181 BP.
XX
AC AAC12537;
XX
DT 06-OCT-2000 (first entry)
XX
DE Human secreted protein 5' EST, SEQ ID NO: 16612.
XX
KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KW gene therapy; chromosome mapping; ss.
XX
OS Homo sapiens.
XX
PN EP1033401-A2.
XX
PD 06-SEP-2000.
XX

PF 21-FEB-2000; 2000EP-00200610.
 XX
 PR 26-FEB-1999; 99US-0122487P.
 XX
 PA (GEST) GENSET.
 XX
 PI Dumas Milne Edwards J, Duclert A, Giordano J;
 XX
 DR WPI; 2000-500381/45.
 XX
 PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for
 PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
 PT diagnostic, forensic, gene therapy and chromosome mapping procedures.
 XX
 PS Claim 1; SEQ ID NO 16612; 71pp + Sequence Listing; English.
 XX
 CC The present sequence is one of a large number of 5' ESTs derived from
 CC mRNAs encoding secreted proteins. No ORF has yet been conclusively
 CC identified within the present sequence. The 5' ESTs were prepared from
 CC total human RNAs or polyA+ RNAs derived from 30 different tissues. EST
 CC sequences usually correspond mainly to the 3' untranslated region (UTR)
 CC of the mRNA because they are often obtained from oligo-dT primed cDNA
 CC libraries. Such ESTs are not well suited for isolating cDNA sequences
 CC derived from the 5' ends of mRNAs and even in those cases where longer
 CC cDNA sequences have been obtained, the full 5' UTR is rarely included. 5'
 CC ESTs are derived from mRNAs with intact 5' ends and can therefore be used
 CC to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in
 CC diagnostic, forensic, gene therapy and chromosome mapping procedures.
 CC They are used to obtain upstream regulatory sequences and to design
 CC expression and secretion vectors
 XX
 SQ Sequence 181 BP; 35 A; 35 C; 92 G; 19 T; 0 U; 0 Other;
 OY Query Match 16.1%; Score 24.8; DB 3; Length 181;
 Best Local Similarity 67.3%; Pred. No. 5.4e+03;
 Matches 35; Conservative 0; Mismatches 17; Indels 0; Gaps 0;
 Db 79 CGCCGACTGCAGATGAGCGGATGACCACTCCGGCCCGACTCGACGAT 130
 71 CGCCGCCCGCGGAGAGAGCGGAGCGGCTCGCGCCCGCGAGAGTAGGGGAT 20
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 ID ADS69652 standard; cDNA; 164 BP.
 XX
 AC ADS69652;
 XX
 DT 18-NOV-2004 (first entry)
 XX
 DE Corn seedling-derived polynucleotide (cpds), SEQ ID 4668.
 XX
 KW Corn; seedling-derived polynucleotide; cdp; ss; plant; seed growth;
 KW seed development; disease resistance; insect infestation; fungal disease;
 KW bacterial infection; Goss' Bacterial Wilt; blight;
 KW Stewart's bacterial Wilt; Holcus spot; bacterial leaf blight; leaf spot;
 KW bacterial stripe; maize dwarf mosaic virus infection;
 KW environmental stress; water stress; pH stress; temperature stress;
 KW pollution; injury; pesticide.
 XX
 OS Zea mays.
 XX
 PN US2003237110-A9.
 XX
 PD 25-DEC-2003.
 XX
 PF 06-AUG-2001; 2001US-00923876.
 XX
 PR 12-MAY-1998; 98US-0085331P.
 PR 21-APR-1999; 99US-00298329.
 XX
 PA (INCY-) INCYTE PHARM INC.
 XX

PI Lalgudi RV, Ito LY, Sherman BK;
 XX
 DR WPI; 2002-195165/25.
 XX
 PT New corn seedling-derived polynucleotides and polypeptides, useful in
 PT identifying and altering desired characteristics associated with growth
 PT and development, disease resistance, environmental adaptability, quality
 PT and yield.
 XX
 PS Claim 1; SEQ ID NO 4668; 33pp; English.
 XX
 CC The invention relates to a corn seedling-derived polynucleotide (cdp)
 CC selected from ADS64985-ADS71316, or their complements and fragments. Also
 CC included are a composition for the detection of altered expression of a
 CC cdp (comprising a polynucleotide selected from ADS64985-ADS71316), a
 CC method of detecting a polynucleotide in a biological sample using a cdp,
 CC a method for using oligomers (and amplification) to recover a regulatory
 CC element from a DNA library using oligomers designed against a cdp, a
 CC seedling specific regulatory element that regulates the expression of a
 CC cdp, an expression vector containing a cdp or regulatory element, a plant
 CC transformed with the vector, a host cell containing the vector (and
 CC expressing a corn seedling derived protein, CDP), an anti-CDP antibody,
 CC identifying a compound which binds a CDP and screening a plurality of
 CC compounds for binding to cdp polynucleotide. The cdp polynucleotides,
 CC proteins, vectors, cells and antibodies are useful for the
 CC identification, evaluation and alteration of seed growth and development,
 CC disease resistance (e.g. to insect infestation, fungal disease, bacterial
 CC infection, Goss' Bacterial Wilt, blight, Stewart's bacterial Wilt, Holcus
 CC spot, bacterial leaf blight, leaf spot, bacterial stripe and maize dwarf
 CC mosaic virus infection) and resistance to environmental stress (e.g.
 CC water stress, pH stress, temperature stress, pollution, injury or
 CC pesticides. The present sequence is cdp cDNA sequence.
 XX
 SQ Sequence 164 BP; 28 A; 53 C; 38 G; 44 T; 0 U; 1 Other;
 OY Query Match 15.8%; Score 24.4; DB 7; Length 164;
 Best Local Similarity 60.6%; Pred. No. 6.7e+03;
 Matches 40; Conservative 0; Mismatches 26; Indels 0; Gaps 0;
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 74 CTGACGACGATGCGGAGCGGATGTCGGCATCTGCTGCGCGCCCTTCCCATCTT 133
 OY 82 CGACTC 87
 Db 134 CTTCTC 139
 RESULT 44
 ADS69652/c
 ID ADS69652 standard; cDNA; 164 BP.
 XX
 AC ADS69652;
 XX
 DT 18-NOV-2004 (first entry)
 XX
 DE Corn seedling-derived polynucleotide (cpds), SEQ ID 4668.
 XX
 KW Corn; seedling-derived polynucleotide; cdp; ss; plant; seed growth;
 KW seed development; disease resistance; insect infestation; fungal disease;
 KW bacterial infection; Goss' Bacterial Wilt; blight;
 KW Stewart's bacterial Wilt; Holcus spot; bacterial leaf blight; leaf spot;
 KW bacterial stripe; maize dwarf mosaic virus infection;
 KW environmental stress; water stress; pH stress; temperature stress;
 KW pollution; injury; pesticide.
 XX
 OS Zea mays.
 XX
 PN US2003237110-A9.
 XX
 PD 25-DEC-2003.
 XX
 PF 06-AUG-2001; 2001US-00923876.
 XX

XX 12-MAY-1998; 98US-0085331P.
 PR 21-APR-1999; 99US-00298329.
 XX
 PA (INCY-) INCYTE PHARM INC.
 XX
 PI Lalgudi RV, Ito LY, Sherman BK;
 XX
 DR WPI; 2002-195165/25.
 XX
 PT New corn seedling-derived polynucleotides and polypeptides, useful in
 PT identifying and altering desired characteristics associated with growth
 PT and development, disease resistance, environmental adaptability, quality
 PT and yield.
 XX
 PS Claim 1; SEQ ID NO 4668; 33pp; English.
 XX
 CC The invention relates to a corn seedling-derived polynucleotide (cdp)
 CC selected from ADS64985-ADS71316, or their complements and fragments. Also
 CC included are a composition for the detection of altered expression of a
 CC cdp (comprising a polynucleotide selected from ADS64985-ADS71316), a
 CC method of detecting a polynucleotide in a biological sample using a cdp,
 CC a method for using oligomers (and amplification) to recover a regulatory
 CC element from a DNA library using oligomers designed against a cdp, a
 CC seedling specific regulatory element that regulates the expression of a
 CC cdp, an expression vector containing a cdp or regulatory element, a plant
 CC transformed with the vector, a host cell containing the vector (and
 CC expressing a corn seedling derived protein, CDP), an anti-CDP antibody,
 CC identifying a compound which binds a CDP and screening a plurality of
 CC compounds for binding to cdp polynucleotide. The cdp polynucleotides,
 CC proteins, vectors, cells and antibodies are useful for the
 CC identification, evaluation and alteration of seed growth and development,
 CC disease resistance (e.g. to insect infestation, fungal disease, bacterial
 CC infection, Goss' Bacterial Wilt, blight, Stewart's bacterial wilt, Holcus
 CC spot, bacterial leaf blight, leaf spot, bacterial stripe and maize dwarf
 CC mosaic virus infection) and resistance to environmental stresses (e.g.
 CC water stress, pH stress, temperature stress, pollution, injury or
 CC pesticides. The present sequence is cdp cDNA sequence.
 CC
 XX
 SQ Sequence 164 BP; 28 A; 53 C; 38 G; 44 T; 0 U; 1 Other;
 XX
 QY Query Match
 Best Local Similarity 15.8%; Score 24.4; DB 7; Length 164;
 Matches 40; Conservative 0; Mismatches 26; Indels 0; Gaps 0;
 QY 68 GAGTCGGCGCCGCGACTCGACGATGAGCGAGATGACCGCTCCGCCCGCGACTCGAC 127
 Db 139 GAGAGAGATGGCGGAGCGCGCGACGACGAGATGCCGCTTCCGCATCGTC 80
 QY 128 GATGAG 133
 Db 79 GTCGAG 74
 XX
 RESULT 45
 AAI27481
 ID AAI27481 standard; DNA; 185 BP.
 XX
 AC AAI27481;
 XX
 DT 12-OCT-2001 (first entry)
 XX
 DE Probe #17414 for gene expression analysis in human cervical cell sample.
 XX
 KW Probe; human; microarray; gene expression; cervical epithelial cell;
 KW cervical cancer; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200157278-A2.
 XX
 PD 09-AUG-2001.
 XX

PF 30-JAN-2001; 2001WO-US000670.
 XX
 PR 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX
 PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX
 DR WPI; 2001-488901/53.
 XX
 PT Human genome-derived single exon nucleic acid probes useful for analyzing
 PT gene expression in human cervical epithelial cells.
 XX
 PS Claim 25; SEQ ID NO 17414; 487pp; English.
 XX
 CC The present invention relates to human single exon nucleic acid probes
 CC (SENP). The present sequence is one such probe. The SENPs are derived
 CC from human HeLa cells. The SENPs can be used to produce a single exon
 CC microarray, which can be used for measuring human gene expression in a
 CC sample derived from human cervical epithelial cells. By measuring gene
 CC expression, the probes are therefore useful in grading and/or staging of
 CC diseases of the cervix, notably cervical cancer. Note: The sequence data
 CC for this patent did not form part of the printed specification, but was
 CC obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 CC
 XX
 SQ Sequence 185 BP; 30 A; 65 C; 61 G; 29 T; 0 U; 0 Other;
 XX
 QY Query Match
 Best Local Similarity 15.8%; Score 24.4; DB 4; Length 185;
 Matches 76; Conservative 0; Mismatches 61; Indels 5; Gaps 1;
 QY 1 CGCGCGAGCTGTGTCATCTGCTCATCTGTCGAGTCGCGGC-----CGAGCTGTGTCATC 55
 Db 19 CGGCGGGGCTGGCCATGCGCGCTGAGCGGGTCCACCGAGCCCTGCGCGAGCTGTTCATC 78
 QY 56 TCGCTCATCTGTCGAGTCGCGCGCGCGCGCGACTCGACGATGAGCGAGATGACCGCTCCGCGC 115
 Db 79 TCTTCATCGCGGTAGTGGGCAACCGCGAGCAACCGACGACAGCGCCCACTTCTTT 138
 QY 116 CGCGACTCGACGATGAGCGAG 137
 Db 139 GAGTTTCTACCAAGAGGCTAG 160

Search completed: April 9, 2005, 01:10:46
 Job time : 431 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 8, 2005, 23:58:47 ; Search time 1842 Seconds
(without alignments)
4051.088 Million cell updates/sec

Title: US-09-887-194A-13
Perfect score: 154
Sequence: 1 cggcgcgagctgtcatctc.....gagatgaccagctccgccc 154

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 2805242

Minimum DB seq length: 0
Maximum DB seq length: 200

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

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1: gb_ba:*
2: gb_htg:*
3: gb_in:*
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5: gb_ov:*
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8: gb_pl:*
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12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	154	100.0	154	6	AX367128 Sequence
2	154	100.0	154	6	AX367128 Sequence
3	154	100.0	154	6	AX392336 Sequence
4	154	100.0	154	6	AX392336 Sequence
5	80	51.9	80	6	AX367127 Sequence
6	80	51.9	80	6	AX367127 Sequence
7	80	51.9	80	6	AX392335 Sequence
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9	80	51.9	92	6	AX367129 Sequence
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11	29.4	19.1	194	6	AX047784 Sequence
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14	28	18.2	197	6	AR251294 Sequence
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20	26.6	17.3	165	1	AB164172	AB164172 Unculture
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22	26.6	17.3	190	6	AX393057	AX393057 Sequence
23	26.6	17.3	195	6	AX898116	AX898116 Sequence
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27	26.2	17.0	171	6	AR427779	AR427779 Sequence
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32	26.2	17.0	171	6	BD123332	BD123332 EST and e
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37	25.6	16.6	183	6	A58814	A58814 Sequence 3
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47	25	16.2	189	1	AY271325	AY271325 Mycobacte
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67	24.4	15.8	185	6	CQ238242	CQ238242 Sequence
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87	23.8	15.5	98	1	RCAPRKAA	M28006 R.sphaeroid
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92	23.8	15.5	193	9	AF279906	AF279906 Homo sapi

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95 23.6 15.3 71 6 BD035419 Sequence
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97 23.6 15.3 171 6 CQ725345 Sequence
c 98 23.6 15.3 171 6 CQ725345 Sequence
99 23.2 15.1 101 11 BV167402 Sequence
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ALIGNMENTS

RESULT 1
AX367128

LOCUS AX367128 154 bp DNA linear PAT 16-FEB-2002
DEFINITION Sequence 13 from Patent WO0200904.
ACCESSION AX367128
VERSION AX367128.1 GI:18855329

KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.

REFERENCE

1 Glassman,K.F., Gordon-Kamm,W.J., Kinney,A.J., Lowe,K., Stecca,K.L. and Nichols,S.E.
TITLE Recombinant constructs and their use in reducing gene expression
JOURNAL Patent: WO 0200904-A 13 03-JAN-2002;
E. I. du Pont de Nemours and Company (US) ; PIONEER HI-BRED
INTERNATIONAL, INC. (US)

FEATURES

source
1. .154
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="ELVISLIVES complementary region of pKS133"

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 1.1e-19;
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QY 1 CGGCCGAGCTGGTCACTCTCGCTCATCTCGAGTCGGCGCGGAGCTGTCTATCTCGCT 60
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QY 121 ACTCGACGATGAGCGAGATGACCACTCCGCGCG 154
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RESULT 2

AX367128/c AX367128 154 bp DNA linear PAT 16-FEB-2002
DEFINITION Sequence 13 from Patent WO0200904.
ACCESSION AX367128
VERSION AX367128.1 GI:18855329

KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.

REFERENCE

1 Glassman,K.F., Gordon-Kamm,W.J., Kinney,A.J., Lowe,K., Stecca,K.L. and Nichols,S.E.
TITLE Recombinant constructs and their use in reducing gene expression
JOURNAL Patent: WO 0200904-A 13 03-JAN-2002;
E. I. du Pont de Nemours and Company (US) ; PIONEER HI-BRED
INTERNATIONAL, INC. (US)
FEATURES Location/Qualifiers

source

1. .154
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="ELVISLIVES complementary region of pKS133"

ORIGIN

Query Match 100.0%; Score 154; DB 6; Length 154;
Best Local Similarity 100.0%; Pred. No. 1.1e-19;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGCCGAGCTGGTCACTCTCGCTCATCTCGAGTCGGCGCGGAGCTGTCTATCTCGCT 60
DB 154 CGGCCGAGCTGGTCACTCTCGCTCATCTCGAGTCGGCGCGGAGCTGTCTATCTCGCT 95
QY 61 CATCGTCGAGTCGGCGCGCGCGCGGAGTCGACGATGAGCGAGATGACCACTCCGCGCGCG 120
DB 94 CATCGTCGAGTCGGCGCGCGCGCGGAGTCGACGATGAGCGAGATGACCACTCCGCGCGCG 35
QY 121 ACTCGACGATGAGCGAGATGACCACTCCGCGCG 154
DB 34 ACTCGACGATGAGCGAGATGACCACTCCGCGCG 1

RESULT 3

AX392336 AX392336 154 bp DNA linear PAT 23-MAR-2002
LOCUS AX392336
DEFINITION Sequence 25 from Patent WO0216565.
ACCESSION AX392336
VERSION AX392336.1 GI:19700689

KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.

REFERENCE

1 Booth,J.R., Cahoon,R.E., Hitz,W.D., Kinney,A.J. and Yadav,N.S.
TITLE Nucleotide sequences of a new class of diverged delta-9
JOURNAL steroyl-acp desaturase genes
Patent: WO 0216565-A 25 28-FEB-2002;
E. I. du Pont de Nemours and Company (US)

FEATURES

source
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/organism="synthetic construct"
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ORIGIN

Query Match 100.0%; Score 154; DB 6; Length 154;
Best Local Similarity 100.0%; Pred. No. 1.1e-19;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGCCGAGCTGGTCACTCTCGCTCATCTCGAGTCGGCGCGGAGCTGTCTATCTCGCT 60
DB 1 CGGCCGAGCTGGTCACTCTCGCTCATCTCGAGTCGGCGCGGAGCTGTCTATCTCGCT 60
QY 61 CATCGTCGAGTCGGCGCGCGCGCGGAGTCGACGATGAGCGAGATGACCACTCCGCGCGCG 120
DB 61 CATCGTCGAGTCGGCGCGCGCGCGGAGTCGACGATGAGCGAGATGACCACTCCGCGCGCG 120
QY 121 ACTCGACGATGAGCGAGATGACCACTCCGCGCG 154
DB 121 ACTCGACGATGAGCGAGATGACCACTCCGCGCG 154

RESULT 4

AX392336/c AX392336 154 bp DNA linear PAT 23-MAR-2002
LOCUS AX392336
DEFINITION Sequence 25 from Patent WO0216565.
ACCESSION AX392336
VERSION AX392336.1 GI:19700689

KEYWORDS synthetic construct
SOURCE synthetic construct

ORGANISM synthetic construct

other sequences; artificial sequences.

REFERENCE

1

Booth,J.R., Cahoon,R.E., Hitz,W.D., Kinney,A.J. and Yadav,N.S.
Nucleotide sequences of a new class of diverged delta-9

JOURNAL

Patent: WO 0216565-A 25 28-FEB-2002;
E. I. du Pont de Nemours and Company (US)

FEATURES

Location/Qualifiers

1..154

/organism="synthetic construct"

/mol_type="unassigned DNA"

/db_xref="taxon:32630"

/note="ELVISLIVES complementary region of pKS133"

ORIGIN

Query Match 100.0%; Score 154; DB 6; Length 154;

Best Local Similarity 100.0%; Pred. No. 1.1e-19; Mismatches 0; Indels 0; Gaps 0;

Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 154 CGGCCGAGCTGTCATCTCGCTCATCTGTCGAGTCGGCGCCGCGAGCTGTCTATCTCGCT 95

QY 61 CATCTCGAGTCGGCGCCGCGAGCTCGACGATGACGACGATGACGACGACTCCGCGCCG 120

Db 94 CATCTCGAGTCGGCGCCGCGAGCTCGACGATGACGACGATGACGACGACTCCGCGCCG 35

QY 121 ACTGACGATGACGACGATGACGACGACTCCGCGCCG 154

Db 34 ACTGACGATGACGACGATGACGACGACTCCGCGCCG 1

RESULT 5

AX367127

LOCUS AX367127 80 bp DNA linear PAT 16-FEB-2002

DEFINITION Sequence 12 from Patent WO0200904.

ACCESSION AX367127

VERSION AX367127.1 GI:18855328

KEYWORDS

SOURCE synthetic construct

ORGANISM synthetic construct

REFERENCE other sequences; artificial sequences.

AUTHORS

1 Glassman,K.F., Gordon-Kamm,W.J., Kinney,A.J., Lowe,K., Stecca,K.L.
and Nichols,S.E.

TITLE Recombinant constructs and their use in reducing gene expression

JOURNAL Patent: WO 0200904-A 12 03-JAN-2002;
E. I. du Pont de Nemours and Company (US) ; PIONEER HI-BRED

INTERNATIONAL, INC. (US)

FEATURES Location/Qualifiers

source 1..80

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/mol_type="unassigned DNA"

/db_xref="taxon:32630"

/note="ELVISLIVES complementary region of pKS106 and
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Query Match 51.9%; Score 80; DB 6; Length 80;

Best Local Similarity 100.0%; Pred. No. 1.3e-05; Mismatches 0; Indels 0; Gaps 0;

Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 CGGCCGAGCTGTCATCTCGCTCATCTGTCGAGTCGGCGCCGCGAGCTCGACGATGAGC 97

Db 1 CGGCCGAGCTGTCATCTCGCTCATCTGTCGAGTCGGCGCCGCGAGCTCGACGATGAGC 60

QY 98 GAGATGACGACTCCGCGCCG 117

Db 61 GAGATGACGACTCCGCGCCG 80

RESULT 6

AX367127/c

LOCUS AX367127 80 bp DNA linear PAT 16-FEB-2002

DEFINITION Sequence 12 from Patent WO0200904.

ACCESSION AX367127

VERSION AX367127.1 GI:18855328

KEYWORDS

SOURCE synthetic construct

ORGANISM synthetic construct

REFERENCE other sequences; artificial sequences.

AUTHORS

1 Glassman,K.F., Gordon-Kamm,W.J., Kinney,A.J., Lowe,K., Stecca,K.L.
and Nichols,S.E.

TITLE Recombinant constructs and their use in reducing gene expression

JOURNAL Patent: WO 0200904-A 12 03-JAN-2002;
E. I. du Pont de Nemours and Company (US) ; PIONEER HI-BRED

INTERNATIONAL, INC. (US)

FEATURES

source Location/Qualifiers

1..80

/organism="synthetic construct"

/mol_type="unassigned DNA"

/db_xref="taxon:32630"

/note="ELVISLIVES complementary region of pKS106 and
pKS124"

ORIGIN

Query Match 51.9%; Score 80; DB 6; Length 80;

Best Local Similarity 100.0%; Pred. No. 1.3e-05; Mismatches 0; Indels 0; Gaps 0;

Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 CGGCCGAGCTGTCATCTCGCTCATCTGTCGAGTCGGCGCCGCGAGCTCGACGATGAGC 97

Db 80 CGGCCGAGCTGTCATCTCGCTCATCTGTCGAGTCGGCGCCGCGAGCTCGACGATGAGC 21

RESULT 7

AX392335

LOCUS AX392335 80 bp DNA linear PAT 23-MAR-2002

DEFINITION Sequence 24 from Patent WO0216565.

ACCESSION AX392335

VERSION AX392335.1 GI:19700688

KEYWORDS

SOURCE synthetic construct

ORGANISM synthetic construct

REFERENCE other sequences; artificial sequences.

AUTHORS

1 Booth,J.R., Cahoon,R.E., Hitz,W.D., Kinney,A.J. and Yadav,N.S.
Nucleotide sequences of a new class of diverged delta-9

TITLE stearyl-acp desaturase genes

JOURNAL Patent: WO 0216565-A 24 28-FEB-2002;
E. I. du Pont de Nemours and Company (US)

INTERNATIONAL, INC. (US)

FEATURES Location/Qualifiers

source 1..80

/organism="synthetic construct"

/mol_type="unassigned DNA"

/db_xref="taxon:32630"

/note="ELVISLIVES complementary region of pKS106 and
pKS124"

ORIGIN

Query Match 51.9%; Score 80; DB 6; Length 80;

Best Local Similarity 100.0%; Pred. No. 1.3e-05; Mismatches 0; Indels 0; Gaps 0;

Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 CGGCCGAGCTGTCATCTCGCTCATCTGTCGAGTCGGCGCCGCGAGCTCGACGATGAGC 97

Db 1 CGGCCGAGCTGTCATCTCGCTCATCTGTCGAGTCGGCGCCGCGAGCTCGACGATGAGC 60

QY 98 GAGATGACGACTCCGCGCCG 117

Db 61 GAGATGACGACTCCGCGCCG 80

RESULT 6

Db 22 CGAGCTGCGGAAGAGCCTGCTGCGCCTCTCATCATCCACAGCGCCACACCCATGT 81
QY 90 CGATGAGGAGATGACCACTCCGGCC 116
Db 82 CGCTGCCCAAGACACCAAGACCGGCC 108

RESULT 12
AX047784/c 194 bp DNA linear PAT 15-DEC-2000

LOCUS AX047784
DEFINITION Sequence 16 from Patent WO0070044.
ACCESSION AX047784
VERSION AX047784.1 GI:11876790
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS 1 Miltman, S.T. and Agnew, W.S.
TITLE Human brain t calcium channel alpha-subunit splice variants
JOURNAL Patent: WO 0070044-A 16 23-NOV-2000;
FEATURES location/Qualifiers
source 1. .194
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 19.1%; Score 29.4; DB 6; Length 194;
Best Local Similarity 58.6%; Pred. No. 4.1e+04;
Matches 51; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

QY 39 GGCCGAGCTGGTCATCTCGTCAATCGAGTCGGCGCCCGACTCGACGATGAGCG 98
Db 108 GGCCCGTGTGCTCTTGGGAGCAGATGGTGTGGCGCCGTGTGATGATGAGAG 49
QY 99 AGATGACCACTCCGGCCCGCACTCG 125
Db 48 GCGGCAGCAGGCTCTTCGCACTCCG 22

RESULT 13
AR251294

LOCUS AR251294 197 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 6653 from patent US 6476212.
ACCESSION AR251294
VERSION AR251294.1 GI:27299168
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 197)
AUTHORS Lalgudi, R.V., Ito, L.Y. and Sherman, B.K.
TITLE Polynucleotides and polypeptides derived from corn ear
JOURNAL Patent: US 6476212-A 6653 05-NOV-2002;
FEATURES location/Qualifiers
source 1. .197
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 18.2%; Score 28; DB 6; Length 197;
Best Local Similarity 51.2%; Pred. No. 7.6e+04;
Matches 64; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

QY 28 GTCGAGTCGGCGCCGAGCTGTATCTCGCTCATCGTCAGTCGGCGCCCGCACTC 87
Db 63 GCGCGGTGTCCGCCGATCTGCTTGCCTCCGACGACGCTTTAATCCTCCTCAGTCTC 122
QY 88 GACGATGAGGAGATGACCACTCCGGCCCGCACTCGACGATGAGCGAGATGACCACT 147

Db 123 AGTCAGAGCAAGATGGTGCCGCGCGCAGATGACCGAAGAGCGGAGAAACAGGA 182
QY 148 CCGGC 152
Db 183 GCAGC 187

RESULT 14
AR251294/c 197 bp DNA linear PAT 20-DEC-2002

LOCUS AR251294
DEFINITION Sequence 6653 from patent US 6476212.
ACCESSION AR251294
VERSION AR251294.1 GI:27299168
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 197)
AUTHORS Lalgudi, R.V., Ito, L.Y. and Sherman, B.K.
TITLE Polynucleotides and polypeptides derived from corn ear
JOURNAL Patent: US 6476212-A 6653 05-NOV-2002;
FEATURES location/Qualifiers
source 1. .197
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 18.2%; Score 28; DB 6; Length 197;
Best Local Similarity 51.2%; Pred. No. 7.6e+04;
Matches 64; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

QY 3 GCGGAGCTGTGTCATCTCGTCAATCGAGTCGGCGCCCGAGCTGTATCTCGCTCA 62
Db 187 GCTGCTCTGCTTCTCCGCTCTTCTCGTCACTGCCCCGCCACCACTTGTCTCC 128
QY 63 TCGTCAGTCGGCGCCCGCACTCGACGATGACGAGATGACCACTCCGCGCCGAC 122
Db 127 TGACTGAGACTGAGAGANGTAACAGCTGCGTGGGGCAGACAGATCGGGCGACACC 68
QY 123 TCGAC 127
Db 67 GCGCC 63

RESULT 15
AFU557755

LOCUS AFU557755 191 bp DNA linear PLN 19-APR-2004
DEFINITION Aspergillus fumigatus ITS1, isolate 8.
ACCESSION AJ557755
VERSION AJ557755.1 GI:46406330
KEYWORDS internal transcribed spacer 1; ITS1.
SOURCE Aspergillus fumigatus
ORGANISM Aspergillus fumigatus

REFERENCE 1
AUTHORS Hain, M.
TITLE Detection and identification of fungi from bryozoa
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 191)
AUTHORS Hain, M.
TITLE Direct Submission
JOURNAL Submitted (18-APR-2003) Hain M., ICBM, Carl v. Ossietzky
Universitaet Oldenburg, C. v. O. Strasse 9-11, D-26111 Oldenburg,
GERMANY

FEATURES
source

location/Qualifiers
1. .191
/organism="Aspergillus fumigatus"
/mol_type="genomic DNA"
/isolate="g"
/specific_host="Alcyonidium gelatinosum"
/db_xref="taxon:5085"
/country="Germany:North Sea around the island of

[illegible]

Db	Query Match	Best:Local Similarity	Score	DB 1;	Length	165;
QY	24	17.3%;	56.2%;	Pred. No. 1.4e+05;	Mismatches 39;	Indels 0;
DB	160	50;	Conservative 0;	Mismatches 39;	Indels 0;	Gaps 0;
QY	84	17.3%;	Score 26.6;	DB 1;	Length 165;	
DB	100	50;	Conservative 0;	Mismatches 39;	Indels 0;	Gaps 0;
RESULT 21	AX393057	190 bp	DNA	linear	PAT 23-MAR-2002	
LOCUS	AX393057	Sequence 2 from Patent WO0206313.				
DEFINITION	AX393057					
ACCESSION	AX393057					
VERSION	AX393057.1	GI:19701113				
KEYWORDS						
SOURCE	Homo sapiens (human)					
ORGANISM	Homo sapiens					
REFERENCE	1	Kossida, S.				
AUTHORS	1	Regulation of human glutamate receptor delta-1 subunit				
TITLE	Patent: WO 0206313-A 2 24-JAN-2002;					
JOURNAL	Bayer Aktiengesellschaft (DE)					
FEATURES	Location/Qualifiers					
source	1..190					
ORIGIN	/organism="Homo sapiens"					
	/mol_type="unassigned DNA"					
	/db_xref="taxon:9606"					
Query Match	17.3%;	Score 26.6;	DB 6;	Length 190;		
Best Local Similarity	60.3%;	Pred. No. 1.4e+05;				
Matches	44;	Conservative 0;	Mismatches 29;	Indels 0;	Gaps 0;	
QY	60	17.3%;	Score 26.6;	DB 6;	Length 190;	
DB	20	44;	Conservative 0;	Mismatches 29;	Indels 0;	Gaps 0;

QY	120	GACTCGACGATGA	132
Db	80	GCCTCAACGATGA	92

RESULT 22			
AX393057/c			
LOCUS	AX393057	190 bp	DNA
DEFINITION	Sequence 2 from Patent WO0206313.		linear PAT 23-MAR-2002

ALIMURDS	Homo sapiens (human)
SOURCE	Homo sapiens
ORGANISM	Homo sapiens

REFERENCE	1
AUTHORS	Kossida, S.
TITLE	Regulation of human glutamate receptor delta-1 subunit
JOURNAL	Patent: WO 0206313-A 2 24-JAN-2002;

ORIGIN

Query Match	17.3%	Score 26.6;	DB 6;	Length 190;
Best Local Similarity	60.3%;	Pred. No. 1.4e+05;		
Matches 44;	Conservative 0;	Mismatches 29;	Indels 0;	Gaps 0;

Dy
Db

23 TCATCGTCGAGTCCGCCGCCGAGCTGTCAATCTGGTCATACGTGCAGTCGGCGGCCGCC 82
||||| |||| | ||| ||| ||| ||| ||| |||
92 TCATCGTTGAGGCTCAGGTCGGAATCCGCCAATCGAACACCTGTGTCTCTTGCGCCGCG 33

QY	83	GACTCGACGATGA	95
Db	32	TTCTCCTCGAGA	20

RESULT 23					
AX898116					
LOCUS	AX898116	195 bp	DNA	linear	PAT 18-DEC-2003
DEFINITION	Sequence	13979	from Patent	EP1033401.	
ACCESSION	AX898116				
VERSION	AX898116.1	GI:40053029			

REFERENCE
AUTHORS
TITLE
JOURNAL

1
Dumas Milne Edwards, J.B., Duclert, A. and Giordano, J.Y.
Expressed sequence tags and encoded human proteins
Patent: EP 1033401-A 13979 06-SEP-2000;
Genset (FR)

ORIGIN

Query Match	17.3%;	Score 26.6;	DB 6;	Length 195;
Best Local Similarity	56.2%;	Pred. No. 1.4e+05;		
Matches 50;	Conservative	0;	Mismatches 39;	Indels 0;
				Gaps 0;

[illegible]

97 CGAGATGACCACTCCGGCCGCCGACTCG 125

Db 106 CTACGTCCCAAGCTCAGCGCGGCTCG 134

RESULT 24			
AX898116/c			
LOCUS	AX898116	195 bp	DNA
DEFINITION	Sequence	13979 from Patent EP1033401.	linear
ACCESSION	AX898116		
VERSION	AX898116.1	GI:40053029	PAT 18-DEC-2003

SOURCE ORGANISM	
Homo sapiens (human)	
Homo sapiens	
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	

REFERENCE
1
AUTHORS Dumas Milne Edwards, J.B., Duclert, A. and Giordano, J.Y.
TITLE Expressed sequence tags and encoded human proteins
JOURNAL Patent: EP 1033401-A 13979 06-SEP-2000;
Genset (FR)

ORIGIN

Query Match	17.3%	Score 26.6;	DB 6;	Length 195;
Best Local Similarity	56.2%;	Pred. No. 1.4e+05;		
Matches 50; Conservative	0;	Mismatches 39;	Indels 0;	Gaps 0;

[illegible]

QY 90 CGATGAGCGAGATGACCACTCCGGCCGC 118
||| ||| |
Db 74 CGCCGAACGCCAGAACAATGCCCCCAGC 46

RESULT	25			
BD033649				
LOCUS	BD033649	195 bp	DNA	linear
DEFINITION	BD033649	Sequence tag and encoded human protein.		PAT 27-AUG-2002
ACCESSION	BD033649			
VERSION	BD033649.1	GI:22575391		
KEYWORDS	JP 2001269182-A/9895.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			

AUTHORS Edwards, J.B.D.M., Duclair, E. and Jordan, J.Y.
TITLE Sequence tag and encoded human protein
JOURNAL Patent: JP 2001269182-A 9895 02-OCT-2001;

COMMENT	OS	Homo sapiens (human)
	PN	JP 2001269182-A/9895
	PD	02-OCT-2001
	PF	24-FEB-2000 JP 2000118773
	PR	26-FEB-1999 US 60/122487
	PI	JEAN BAPTIST DUMAS MILNE EDWARDS, EIMERIC DUCLAIR, JEAN YVES JORDAN
	PT	JORDAN
	PC	C12N15/09, C07K14/435, C07K16/18, C12N1/15, C12N1/19, C12N1/21, PC C12N5/10,
	PC	C12P21/02, C12P21/08, C12Q1/68//G06F17/30, C12N15/00, C12N5/00, PC G06F15/40

FEATURES

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/organism="Homo sapiens"  
/mol_type="genomic DNA"
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Query Match 17.0%; Score 26.2; DB 6; Length 171;
Best Local Similarity 55.1%; Pred. No. 1.7e+05;
Matches 49; Conservative 1; Mismatches 39; Indels 0; Gaps 0;

OY 30 CGAGTCGGCGCGCGAGCTGTCATCTCGCTCATCTGAGTCGGCGCGCGCGACTCGA 89
|||:|||||
DB 135 CGAKCCGCGCGCTGAGCTGGGACGTAGACCTAGCGCCGAGCCGAGCGAAGAAATCC 76

OY 90 CGATGACGAGATGACCACTCCGCGCCG 118
|||
DB 75 CGCCGACGCGAGACACCGCGCGCAGC 47

RESULT 33

CQ424819 170 bp DNA linear PAT 28-JAN-2004
LOCUS CQ424819
DEFINITION Sequence 9853 from Patent WO0151628.
ACCESSION CQ424819
VERSION CQ424819.1 GI:41377048
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Lillie,J., Xu,Y., Wang,Y. and Steinmann,K.
TITLE Novel genes, compositions, kits, and methods for identification, assessment, prevention, and therapy of breast cancer
JOURNAL Patent: WO 0151628-A 9853 19-JUL-2001;
Millennium Pharmaceuticals, Inc. (US)

FEATURES
source 1..170
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 16.9%; Score 26; DB 6; Length 170;
Best Local Similarity 55.6%; Pred. No. 1.9e+05;
Matches 50; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

OY 61 CATGTCGAGTCGGCGCGCGCGACTCGACGATGAGCGAGATGACCACTCCGCGCGCG 120
|||
DB 18 CTTCGTCGCGCGGTTCTGTCTGATGCGCGCGGTGACGATGGGGCTGCGTCCGCGCGCA 77

OY 121 ACTGACGATGAGCGAGATGACCACTCCG 150
|||
DB 78 GCTCGTCGATCACCGACACTTCCAGGTCGG 107

RESULT 34

CQ424819/c 170 bp DNA linear PAT 28-JAN-2004
LOCUS CQ424819
DEFINITION Sequence 9853 from Patent WO0151628.
ACCESSION CQ424819
VERSION CQ424819.1 GI:41377048
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Lillie,J., Xu,Y., Wang,Y. and Steinmann,K.
TITLE Novel genes, compositions, kits, and methods for identification, assessment, prevention, and therapy of breast cancer
JOURNAL Patent: WO 0151628-A 9853 19-JUL-2001;
Millennium Pharmaceuticals, Inc. (US)

FEATURES
source 1..170
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 16.9%; Score 26; DB 6; Length 170;
Best Local Similarity 55.6%; Pred. No. 1.9e+05;
Matches 50; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

OY 5 CGAGCTGTCATCTCGCTCATCTCGAGTCGGCGCGCGAGCTGTCTATCTCGCTCATC 64
|||
DB 107 CCGACTTGAAGTGTCTGATGACGAGCTGCCGCCCGGACGACGCCCATCTGTACGC 48

OY 65 GTCGAGTCGGCGCGCGCGCGACTCGACGATG 94
|||
DB 47 GCGCCATCGACCGAACCAGCGCGCAGCAAG 18

RESULT 35

CQ416921 189 bp DNA linear PAT 28-JAN-2004
LOCUS CQ416921
DEFINITION Sequence 1955 from Patent WO0151628.
ACCESSION CQ416921
VERSION CQ416921.1 GI:41369150
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Lillie,J., Xu,Y., Wang,Y. and Steinmann,K.
TITLE Novel genes, compositions, kits, and methods for identification, assessment, prevention, and therapy of breast cancer
JOURNAL Patent: WO 0151628-A 1955 19-JUL-2001;
Millennium Pharmaceuticals, Inc. (US)

FEATURES
source 1..189
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 16.9%; Score 26; DB 6; Length 189;
Best Local Similarity 55.6%; Pred. No. 1.8e+05;
Matches 50; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

OY 61 CATGTCGAGTCGGCGCGCGCGACTCGACGATGACCGAGATGACCACTCCGCGCGCG 120
|||
DB 33 CTTCGTCGCGCGGTTCTGTCTGATGCGCGCGGTGACGATGGGGCTGCGTCCGCGCGCA 92

OY 121 ACTGACGATGAGCGAGATGACCACTCCG 150
|||
DB 93 GCTCGTCGATCACCGACACTTCCAGGTCGG 122

RESULT 36

CQ416921/c 189 bp DNA linear PAT 28-JAN-2004
LOCUS CQ416921
DEFINITION Sequence 1955 from Patent WO0151628.
ACCESSION CQ416921
VERSION CQ416921.1 GI:41369150
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Lillie,J., Xu,Y., Wang,Y. and Steinmann,K.
TITLE Novel genes, compositions, kits, and methods for identification, assessment, prevention, and therapy of breast cancer
JOURNAL Patent: WO 0151628-A 1955 19-JUL-2001;
Millennium Pharmaceuticals, Inc. (US)

FEATURES
source 1..189
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

[illegible]

TITLE	A molecular and morphological perspective on the phylogenetic relationships of the otophysan fishes									
JOURNAL	Mol. Phylogenet. Evol. 6 (1), 120-133 (1996)									
MEDLINE	96426866									
PUBMED	8812312									
REFERENCE	2 (bases 1 to 105)									
AUTHORS	Dimmick, W.W. and Larson, A.									
TITLE	Direct Submission									
JOURNAL	Submitted (10-AUG-1995) University of Kansas, Dyche Hall, Jayhawk Boulevard, Lawrence, KS 66045, USA									
FEATURES	Location/Qualifiers									
Source	1..105									
	/organism="Apteronotus leptorhynchus"									
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	/db_xref="taxon:36674"									
	/tissue_type="muscle"									
	/note="AC2854"									
	<1..>105									
	/product="28S ribosomal RNA"									
ORIGIN										
Query Match	16.5%; Score 25.4; DB 5; Length 105;									
Best Local Similarity	60.3%; Pred. No. 2.7e+05;									
Matches	41; Conservative 0; Mismatches 27; Indels 0; Gaps 0;									
QY	68 GAGTCGGCGCGCCGCACTCGACGATGAGCGAGATGACCACTCCGCGCGCACTCGAC 127									
Db	104 GGGTAGCCGGCATCCGCGGTGACCCCGAGCGCCGTACNAGGCGCGGTCCCGCTGGGC 45									
QY	128 GATGAGCG 135									
Db	44 GCGGCGCG 37									
RESULT 43										
ABI64173	165 bp DNA linear BCT 10-MAR-2004									
LOCUS	ABI64173									
DEFINITION	Uncultured bacterium nirS gene for nitrite reductase, partial cds,									
ACCESSION	ABI64173									
VERSION	ABI64173.1 GI:45330786									
KEYWORDS	uncultured bacterium									
SOURCE	uncultured bacterium									
ORGANISM	Bacteria; environmental samples.									
REFERENCE	1									
AUTHORS	Shoji, T.									
TITLE	Microbial communities of an enhanced biological phosphorus removal process using oxygen, nitrate and nitrite as electron acceptors									
JOURNAL	Unpublished									
REFERENCE	2 (bases 1 to 165)									
AUTHORS	Shoji, T.									
TITLE	Direct Submission									
JOURNAL	Submitted (26-FEB-2004) Tadashi Shoji, The University of Tokyo, Department of Urban Engineering, 7-3-1, Hongo, Bunkyo, Tokyo 113-8656, Japan (E-mail: shoji@env.t.u-tokyo.ac.jp, Tel: 81-3-5841-7784, Fax: 81-3-5841-8538)									
FEATURES	Location/Qualifiers									
source	1..165									
	/organism="uncultured bacterium"									
	/mol_type="genomic DNA"									
	/isolate="DGE band f2r5-sa"									
	/isolation_source="activated sludge from lab-scale SBR fed with wastewater"									
	/db_xref="taxon:77133"									
	/environmental_sample									
	/country="Japan:Tokyo"									
	/note="PCR products amplified by primers nirS2fGC and nirS3R were analyzed by DGE"									
	1..165									
	/gene="nirS"									
	<1..>165									
	/gene="nirS"									
gene										
CDS										

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/codon_start=1
/transl_table=11
/product="nitrite reductase"
/protein_id="BAD12411.1"
/db_xref="GI:45330787"
/translation="YHPEPRVASIVASHYKPEFVVNVKETGTLTLDVSNVDALKVT
IGTARFLHDG"
ORIGIN

Query Match      16.5%; Score 25.4; DB 1; Length 165;
Best Local Similarity 58.7%; Pred. No. 2.4e+05;
Matches 44; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 57 CGCTCATGCTCGAGTCGGCGCGCCGCGACTCGACGATGACGAGATGACCACTCCGGCC 116
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 86 CGCTGCTGCTGCTGACTCTGCAACGCTCGACGCGCTGAAGTCAACGACCATCGGACCGCGC 145
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 117 GCCGACTCGACGATG 131
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 146 GCTTCCTGACGACG 160

RESULT 44
ABI64173/c 165 bp DNA linear BCT 10-MAR-2004
LOCUS Uncultured bacterium nirS gene for nitrite reductase, partial cds,
DEFINITION isolate:DGGE band f2r5-sa.
ACCESSION AB164173
VERSION AB164173
KEYWORDS uncultured bacterium
SOURCE uncultured bacterium
ORGANISM Bacteria; environmental samples.

REFERENCE
1 Shoji,T.
  Microbial communities of an enhanced biological phosphorus removal
  process using oxygen, nitrate and nitrite as electron acceptors
  Unpublished
2 (bases 1 to 165)
  Shoji,T.
  Direct Submission
  Submitted (26-FEB-2004) Tadashi Shoji, The University of Tokyo,
  Department of Urban Engineering; 7-3-1, Hongo, Bunkyo, Tokyo
  113-8656, Japan (E-mail:shoji@env.t.u-tokyo.ac.jp,
  Tel:81-3-5841-7784, Fax:81-3-5841-8538)
  Location/Qualifiers
FEATURES
source
1..165
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  /mol_type="genomic DNA"
  /isolate="DGGE band f2r5-sa"
  /isolation_source="activated sludge from lab-scale SBR fed
  with wastewater"
  /db_xref="taxon:77133"
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  1..165
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Query Match      16.5%; Score 25.4; DB 1; Length 165;
Best Local Similarity 58.7%; Pred. No. 2.4e+05;
Matches 44; Conservative 0; Mismatches 31; Indels 0; Gaps 0;
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QY 24 CATGCTGAGTCGGCGCGCGGAGCTGTCATCTCGCTCATCGAGTCGGCGCGCGC 83
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 160 CGTGTGACGAGAAAGCGCGGTGCGCATGTGTCGACCTTCAGCGCGTTCAGCTTCAGT 101
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 84 ACTCGACGATGACG 98
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 100 AGTCGACGACGACG 86

RESULT 45
BD238411
LOCUS Sorting of proteins using RNA-protein fused body.
DEFINITION BD238411
ACCESSION BD238411.1 GI:33048181
VERSION BD238411.1
KEYWORDS JP 2002536025-A/29.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE 1 (bases 1 to 123)
JOURNAL Szostak,J.W., Roberts,R.W. and Liu,R.
  Sorting of proteins using RNA-protein fused body
  Patent: JP 2002536025-A 29 29-OCT-2002;
  THE GENERAL HOSPITAL CORP
COMMENT OS Homo sapiens (human)
PN JP 2002536025-A/29
PD 29-OCT-2002
PF 01-FEB-2000 JP 2000598669
PR 09-FEB-1999 US 09/247190
PI JACK W SZOSTAK,RICHARD W ROBERTS,RIHE LIU
PC C12N15/09,C07K7/00,C07K14/00,C12Q1/68,C12N15/00 CC n = a, g,
  t, or c. s = c or g.
FH Key Location/Qualifiers
FT misc feature (22)..(102).
FEATURES
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ORIGIN

Query Match      16.2%; Score 25; DB 6; Length 123;
Best Local Similarity 15.0%; Pred. No. 3.1e+05;
Matches 16; Conservative 26; Mismatches 65; Indels 0; Gaps 0;
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Search completed: April 9, 2005, 01:41:41
Job time : 1850 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 8, 2005, 21:50:21 ; Search time 3123 Seconds
(without alignments)
1877.008 Million cell updates/sec

Title: US-09-887-194A-13
Perfect score: 154
Sequence: 1 cggccgagctgtgtcatctc.....gagatgaccagctccgcccg 154

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : EST.*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	38.2	24.8	512	8	BZ566906 pac82-164
2	38.2	24.8	512	8	BZ566906 pac82-164
3	38.2	24.8	513	6	CD931316 GR45.114C
4	38.2	24.8	513	6	CD931316 GR45.114C
5	37	24.0	1878	9	CL981398 OsIFCC045
6	37	24.0	1878	9	CL981398 OsIFCC045
7	36.6	23.8	175	4	BF945949 CM0-NN115
8	36.6	23.8	175	4	BF945949 CM0-NN115
9	36.6	23.8	514	6	CD895591 G174.100E
10	36.6	23.8	514	6	CD895591 G174.100E
11	36.4	23.6	653	8	BZ509933 BOMQF14TF
12	36.4	23.6	653	8	BZ509933 BOMQF14TF
13	36.4	23.6	711	8	BH925906 odg84c07.
14	36.4	23.6	711	8	BH925906 odg84c07.
15	36.4	23.6	818	8	BZ427562 BONJT45TR
16	36.4	23.6	818	8	BZ427562 BONJT45TR
17	36.4	23.6	834	9	CL980758 OsIFCC045
18	36.4	23.6	834	9	CL980758 OsIFCC045
19	36.2	23.5	627	9	CNS030BV
20	36.2	23.5	627	9	CNS030BV
21	36.2	23.5	787	8	AZ933792 BJ_Ba000
22	36.2	23.5	787	8	AZ933792 BJ_Ba000
23	36.2	23.5	1057	9	CNS03W2P
24	36.2	23.5	1057	9	CNS03W2P

25	36	23.4	862	7	CO435934	CO435934 OsMR568 5
26	36	23.4	862	7	CO435934	CO435934 OsMR568 5
27	36	23.4	972	9	CNS04TDK	AL306353 Tetraodon
28	36	23.4	972	9	CNS04TDK	AL306353 Tetraodon
29	35.8	23.2	367	5	BQ767987	BQ767987 EBro08_SQ
30	35.8	23.2	367	5	BQ767987	BQ767987 EBro08_SQ
31	35.6	23.1	397	9	CE011375	CE011375 tigr-gss-
32	35.6	23.1	397	9	CE011375	CE011375 tigr-gss-
33	35.6	23.1	624	6	CB682412	CB682412 OsJNEf09L
34	35.6	23.1	624	6	CB682412	CB682412 OsJNEf09L
35	35.6	23.1	677	6	CA198784	CA198784 SCCST3C1
36	35.6	23.1	677	6	CA198784	CA198784 SCCST3C1
37	35.4	23.0	590	1	AI399069	AI399069 NCW01B11T
38	35.4	23.0	590	1	AI399069	AI399069 NCW01B11T
39	35.4	23.0	704	6	CA227997	CA227997 SCJLFL301
40	35.4	23.0	704	6	CA227997	CA227997 SCJLFL301
41	35	22.7	441	2	BF483067	BF483067 WHE2314_D
42	35	22.7	441	2	BF483067	BF483067 WHE2314_D
43	35	22.7	571	5	BQ805125	BQ805125 WHE3563_B
44	35	22.7	571	5	BQ805125	BQ805125 WHE3563_B
45	34.8	22.6	430	4	BG279219	BG279219 b1f04np.r
46	34.8	22.6	430	4	BG279219	BG279219 b1f04np.r
47	34.8	22.6	497	1	AL829848	AL829848 AL829848
48	34.8	22.6	497	1	AL829848	AL829848 AL829848
49	34.8	22.6	558	1	AI397686	AI397686 NCC1D1T3
50	34.8	22.6	558	1	AI397686	AI397686 NCC1D1T3
51	34.8	22.6	673	5	BQ841269	BQ841269 WHE4209_A
52	34.8	22.6	673	5	BQ841269	BQ841269 WHE4209_A
53	34.6	22.5	664	7	CF133957	CF133957 WHE4365_G
54	34.6	22.5	664	7	CF133957	CF133957 WHE4365_G
55	34.6	22.5	1012	9	CNS03D7T	AL238754 Tetraodon
56	34.6	22.5	1012	9	CNS03D7T	AL238754 Tetraodon
57	34.6	22.5	1050	6	CA139626	CA139626 SCEORT210
58	34.6	22.5	1050	6	CA139626	CA139626 SCEORT210
59	34.4	22.3	415	2	BF462402	BF462402 UI-M-CG0P
60	34.4	22.3	415	2	BF462402	BF462402 UI-M-CG0P
61	34.4	22.3	503	2	BF466956	BF466956 UI-M-CG0P
62	34.4	22.3	503	2	BF466956	BF466956 UI-M-CG0P
63	34.4	22.3	569	9	CL950005	CL950005 OsIRUA001
64	34.4	22.3	569	9	CL950005	CL950005 OsIRUA001
65	34.4	22.3	703	5	BU055691	BU055691 UI-M-FOO-
66	34.4	22.3	703	5	BU055691	BU055691 UI-M-FOO-
67	34.4	22.3	769	8	BH555985	BH555985 BOHER70TF
68	34.4	22.3	769	8	BH555985	BH555985 BOHER70TF
69	34.4	22.3	771	8	BH447921	BH447921 BOGHE53TR
70	34.4	22.3	771	8	BH447921	BH447921 BOGHE53TR
71	34.4	22.3	880	7	CN204763	CN204763 Tor5149 G
72	34.4	22.3	880	7	CN204763	CN204763 Tor5149 G
73	34.4	22.3	891	8	BZ571836	BZ571836 msh2_2078
74	34.4	22.3	891	8	BZ571836	BZ571836 msh2_2078
75	34.2	22.2	288	5	BQ756129	BQ756129 EBem05_SQ
76	34.2	22.2	288	5	BQ756129	BQ756129 EBem05_SQ
77	34.2	22.2	500	4	BG366731	BG366731 HVSME1000
78	34.2	22.2	500	4	BG366731	BG366731 HVSME1000
79	34.2	22.2	551	5	BQ464534	BQ464534 HF02122r
80	34.2	22.2	551	5	BQ464534	BQ464534 HF02122r
81	34.2	22.2	600	6	CB689196	CB689196 CEST-45-B
82	34.2	22.2	600	6	CB689196	CB689196 CEST-45-B
83	34.2	22.2	606	5	BU993939	BU993939 HM05A17r
84	34.2	22.2	606	5	BU993939	BU993939 HM05A17r
85	34.2	22.2	645	6	CB688201	CB688201 CEST-10-H
86	34.2	22.2	645	6	CB688201	CB688201 CEST-10-H
87	34.2	22.2	647	4	BI960178	BI960178 HVSME002
88	34.2	22.2	647	4	BI960178	BI960178 HVSME002
89	34.2	22.2	669	1	AU078265	AU078265 AU078265
90	34.2	22.2	669	1	AU078265	AU078265 AU078265
91	34.2	22.2	695	2	BF622282	BF622282 HVSMEa000
92	34.2	22.2	695	2	BF622282	BF622282 HVSMEa000
93	34.2	22.2	783	4	BM816829	BM816829 HC03D11_T
94	34.2	22.2	783	4	BM816829	BM816829 HC03D11_T
95	34.2	22.2	818	2	AW983195	AW983195 HVSMEg000
96	34.2	22.2	818	2	AW983195	AW983195 HVSMEg000
97	34.2	22.2	851	2	BF256658	BF256658 HVSMEf001

c 98 34.2 22.2 851 2 BF256658
99 34.2 22.2 1035 7 CK162563
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ALIGNMENTS

RESULT 1

BZ566906

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Genome Center

University of Washington

Box 352145, Seattle, WA 98105-2145, USA

Tel: 2062216954

Fax: 2066857244

Email: craymond@u.washington.edu

Class: shotgun.

Location/Qualifiers

1..512

/organism="Pseudomonas aeruginosa"

/mol_type="genomic DNA"

/strain="2-164"

/db_xref="taxon:287"

/clone="pacs2-164_6657"

/clone_lib="pacs2-164"

/note="clinical isolate 2-164 whole genomic shotgun library."

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Burns, J.L., Kaul, R. and Olsen, M.V.
Whole-Genome-Sequence variation among multiple isolates of
Pseudomonas aeruginosa library
J. Bacteriol. (2002) In press
Contact: Chris K. Raymond
Genome Center
University of Washington
Box 352145, Seattle, WA 98105-2145, USA
Tel: 2062216954
Fax: 2066857244
Email: craymond@u.washington.edu
Class: shotgun.

ALIGNMENTS

RESULT 1

BZ566906

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Genome Center

University of Washington

Box 352145, Seattle, WA 98105-2145, USA

Tel: 2062216954

Fax: 2066857244

Email: craymond@u.washington.edu

Class: shotgun.

Location/Qualifiers

1..512

/organism="Pseudomonas aeruginosa"

/mol_type="genomic DNA"

/strain="2-164"

/db_xref="taxon:287"

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/note="clinical isolate 2-164 whole genomic shotgun library."

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Query Match	24.8%	Score 38.2;	DB 6;	Length 513;
Best Local Similarity	53.7%	Pred. No. 12;		
Matches 79; Conservative	0;	Mismatches 68;	Indels 0;	Gaps 0;

OY		8	AGCTGGTCATCTCGCTCATCGTGCAGTGCCGCCGGAAGCTGTGTCATTCTCGCTCATCCTC	67
Dd		138	AACGAGGCGTTCCAACACTCTCTCCGCCCAAGCTCGCCCTCGAAGCTGTGCTCACCGTC	197
OY		68	GAGTCGCGCGCGCCGCACTGCAGCATGAGCAGATGACCAGCTCCGCCGCACTCGAC	127
Dd		198	ACCGCAGCCGCCCGCCACGACGACGCGCGAGTCGAGCACCACGACAAGCAACGCGGC	257
OY		128	GATGAGCGAGATGACCAGCTCCGCCG	154
Dd		258	GCGCAGGCCCGCGCCGAGCGCAGCCGCG	284

RESULT 4

LOCUS	CD931316	513 bp	mRNA	linear	EST 15-JUL-2003
DEFINITION	GR45.114C04F010419	GR45	Triticum aestivum	CDNA clone	GR45114C04,
	mRNA sequence.				
ACCESSION	CD931316				
VERSION	CD931316.1	GI:32779080			
KEYWORDS	EST.				
SOURCE	Triticum aestivum (bread wheat)				
ORGANISM	Triticum aestivum				

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1	(bases 1 to 513)	Genoplahte.	Genoplahte, a major partnership french program in plant genomics	Unpublished (2003)
			Contact: Genoplahte	Genoplahte
			93, rue Henri Rochefort 91025 EVRY CEDEX France	
			Tel: 33 1 69 47 54 00	
			Fax: 33 1 69 47 54 10	
			This sequence has been generated in the framework of the french plant genomics programme 'Genoplahte' (http://www.genoplahte.com and http://genoplahte-info.infobiogen.fr).	

FEATURES	Location/Qualifiers
source	1. .513

ORIGIN

Query Match	24.8%	Score 38.2;	DB 6;	Length 513;
Best Local Similarity	54.7%;	Pred. No. 12;		
Matches 76; Conservative	0;	Mismatches 63;	Indels 0;	Gaps 0;

QY	9	GCTGGTCATCTCGCTCATCGTCGAGTCGGCGCCGGAGCTGGTCATCTCGCTCATCGTCG	68
Db	276	GCTCGCGCGCGGCGCTGCGCGCGCGCGCTGTGCTGCGTGCTGCTGCACTCGGCGGTCTCG	217
QY	69	AGTCGCGCGCGCGCGCTCGACGATGACGAGATGACCACTCCGGCCGCACTCGACG	128
Db	216	TGGCGGCGCGCGGTGCGCGGTGACCGGTGACGACAGGTCCAGGGCGGAGCTTGGGGCGGGAGG	157
QY	129	ATGAGCGAGATGACCACT	147
Db	156	AGGTGTGACGCGCTCGTT	138

RESULT 5

CL981398	LOCUS	DEFINITION
CL981398	1878 bp	DNA linear
OSIFCC045611	Oryza sativa Express Library	Oryza sativa (indica cultivar-group) genomic, genomic survey sequence.
GSS 21-SEP-2004		

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FEATURES
  source
    Location/Qualifiers
      1..1878
        /organism="Oryza sativa (indica cultivar-group)"
        /mol_type="genomic DNA"
        /db_xref="taxon:39946"
        /clone_lib="Oryza sativa Express Library"
        /note="Oryza sativa exon trapped genomic sequences"

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ORIGIN

Query Match	24.0%	Score 37;	DB 9;	Length 1878;
Best Local Similarity	53.0%	Pred. No. 23;		
Matches	79;	Conservative	0;	Mismatches 70;
			Indels	0;
			Gaps	0;

[illegible]

RESULT 6

LOCUS	1878 bp	DNA	linear	GSS 21-SEP-2004
DEFINITION	CL981398	Oryza sativa	Express Library	Oryza sativa (indica cultivar-group) genomic, genomic survey sequence.

TITLE
An analysis of transcriptional regulation of the rice genome and its comparison to Arabidopsis

/dev stage="Adult"
/clone_lib="NN1155"
/note="Organ: nervous normal; Vector: puc18; Site 1: Sma1;
Site_2: Sma1; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

ORIGIN

Query Match 23.8%; Score 36.6; DB 4; Length 175;
Best Local Similarity 65.1%; Pred. No. 32;
Matches 54; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 3 GCCGAGCTGTCATCTCGCTCATGTCGAGTCGGCGCGGAGCTGTGTCATCTGCTCA 62
DB 89 GCCCGACGTGTCATTCTCTCACCACTACCGCCCGACGTGTCCTTCCCTCA 30
QY 63 TCCTCGAGTCGGCGCGCGCGAC 85
DB 29 CCACCCAGCCTACCGCCACAGAC 7

RESULT 9

LOCUS CD895591 514 bp mRNA linear EST 14-JUL-2003
DEFINITION G174.100E07F010705 G174 Triticum aestivum cDNA clone G174100E07,
mRNA sequence.

ACCESSION CD895591 GI:32668349
VERSION CD895591.1
KEYWORDS EST.
SOURCE Triticum aestivum (bread wheat)
ORGANISM Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Triticum.

REFERENCE 1 (bases 1 to 514)
Genoplane.

AUTHORS Genoplane, a major partnership french program in plant genomics
TITLE Unpublished (2003)
JOURNAL Contact: Genoplane
COMMENT Genoplane

Genoplane
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10

This sequence has been generated in the framework of the french
plant genomics programme 'Genoplane' (<http://www.genoplane.com>)
and <http://genoplane-info.infobiogen.fr>.

FEATURES
source location/Qualifiers
1..514

/organism="Triticum aestivum"
/mol_type="mRNA"
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/db_xref="taxon:4565"
/clone="G174100E07"
/tissue_type="grain (174 degrees per day after
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ORIGIN

Query Match 23.8%; Score 36.6; DB 6; Length 514;
Best Local Similarity 53.1%; Pred. No. 31;
Matches 78; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

QY 8 AGCTGGTCACTCTGCTCATGTCGAGTCGGCGCGAGCTGTCATCTGCTCATGTC 67
DB 314 AACGAGGCGTCCACACCTCTCCGCGCCCAAGCTCGCCTCGACCTGTGCTCACCGTC 373
QY 68 GAGTCGGCGCGCGCGACTCGACGATGAGCGAGATGACCACTCCGCGCGCGACTCGAC 127
DB 374 ACCGCGACCGCGCGCGCGCGAGGAGCGCGCGAGTCGAGCACCAAGACAGCAAGCGCGGC 433

QY 128 GATGAGCGAGATGACCACTCCGCGC 154
DB 434 GCCAGCGCGCGCGCGAGCGGCGCGG 460

RESULT 10
LOCUS CD895591/c 514 bp mRNA linear EST 14-JUL-2003
DEFINITION G174.100E07F010705 G174 Triticum aestivum cDNA clone G174100E07,
mRNA sequence.

ACCESSION CD895591 GI:32668349
VERSION CD895591.1
KEYWORDS EST.
SOURCE Triticum aestivum (bread wheat)
ORGANISM Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Triticum.

REFERENCE 1 (bases 1 to 514)
Genoplane.

AUTHORS Genoplane, a major partnership french program in plant genomics
TITLE Unpublished (2003)
JOURNAL Contact: Genoplane
COMMENT Genoplane

Genoplane
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10

This sequence has been generated in the framework of the french
plant genomics programme 'Genoplane' (<http://www.genoplane.com>)
and <http://genoplane-info.infobiogen.fr>.

FEATURES
source location/Qualifiers
1..514

/organism="Triticum aestivum"
/mol_type="mRNA"
/cultivar="rectal"
/db_xref="taxon:4565"
/clone="G174100E07"
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pollination)"
/clone_lib="G174"

ORIGIN

Query Match 23.8%; Score 36.6; DB 6; Length 514;
Best Local Similarity 54.0%; Pred. No. 31;
Matches 75; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 9 GCTGTCATCTGCTCATGTCGAGTCGGCGCGGAGCTGTGTCATCTGCTCATGTCG 68
DB 452 GCTCGCGCGCGCGCTGCGCGCGCGCTGTGTCGTGCTGCTGCTGCTGCTGCTGCTG 393
QY 69 AGTCGCGCGCGCGCGACTCGACGATGAGCGAGATGACCACTCCGCGCGCGACTCGACG 128
DB 392 TGGCGCGCGCGCGTGGCGGTGAGCGAGCGACAGCTGAGCGCGAGCTTGGCGCGGAGG 333
QY 129 ATGAGCGAGATGACCACT 147
DB 332 AGTGTGAGACGCTGCTT 314

RESULT 11

LOCUS BZ509933 653 bp DNA linear GSS 16-DEC-2002
DEFINITION BOMQF14TF_BO_2_3_KB Brassica oleracea genomic clone BOMQF14,
genomic survey sequence.

ACCESSION BZ509933
VERSION BZ509933.1
KEYWORDS GSS.
SOURCE Brassica oleracea
ORGANISM Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE 1 (bases 1 to 653)

AUTHORS Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.
TITLE Whole genome shotgun sequencing of Brassica oleracea
JOURNAL Unpublished (2001)
COMMENT Other_GSSs: BOMQF14TR
Contact: Chris Town
TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208

Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TF

Class: sheared ends.

FEATURES
source Location/Qualifiers

1..653
/organism="Brassica oleracea"
/mol_type="genomic DNA"
/strain="TO1000DH3"
/db_xref="taxon:3712"
/clone="BOMQF14"
/clone_lib="BO_2_3_KB"
/note="Vector: pHO51; Site_1: BstXI; 2-3 kb sheared
genomic DNA inserted into pHO51 using BstXI linkers"

ORIGIN

Query Match 23.6%; Score 36.4; DB 8; Length 653;
Best Local Similarity 55.6%; Pred. No. 34;
Matches 70; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 18 CTCGCTCATCGTCAGATCGCGCGCCGAGCTGTCATCTCGTCATCGTCGAGTCGCGG 77
|||||
Db 359 CTCGCCCATGGCGGAGGTGACCTCTGCGCGGGTCTCTCCCTCGCCCATGGCGGAGTGACCA 418
78 CCGCCGACTCGACGATGAGCGAGATGACCACTCCGCGCCGCGACTCGACGATGAGCGAG 137
|||||
Db 419 TGGCGGAGTGACCATGGCGGAGGTGACCTCGGTGCGGGTCTTCTCGCTCAGGGGCGAG 478
QY 138 ATGACC 143
|||||
Db 479 GTGATC 484

RESULT 12 653 bp DNA linear GSS 16-DEC-2002
BZ509933/c BOMQF14TR BO_2_3_KB Brassica oleracea genomic clone BOMQF14,
LOCUS genomic survey sequence.

ACCESSION BZ509933
VERSION BZ509933
KEYWORDS GSS.
SOURCE Brassica oleracea

ORGANISM Brassica oleracea

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 653)
Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.
Whole genome shotgun sequencing of Brassica oleracea
Unpublished (2001)
Other_GSSs: BOMQF14TR
Contact: Chris Town
TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org

DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TF
Class: sheared ends.

FEATURES
source Location/Qualifiers
1..653
/organism="Brassica oleracea"
/mol_type="genomic DNA"

/strain="TO1000DH3"
/db_xref="taxon:3712"
/clone="BOMQF14"
/clone_lib="BO_2_3_KB"
/note="Vector: pHO51; Site_1: BstXI; 2-3 kb sheared
genomic DNA inserted into pHO51 using BstXI linkers"

ORIGIN

Query Match 23.6%; Score 36.4; DB 8; Length 653;
Best Local Similarity 55.6%; Pred. No. 34;
Matches 70; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 12 GGTATCTCGCTCATCGTCAGTGGCGCCGAGCTGTCATCTCGTCATCGTCGAGT 71
|||||
Db 484 GATCACTCGCCCTGAGCGGAGAACCCGACCGAGGTCACTCGCCCATGTCACT 425
72 CGGCGCGCCGACTCGACGATGAGCGAGATGACCACTCCGCGCCGAGCTCGACGATG 131
|||||
Db 424 CGCCCATGTCACTCGCCCATGGCGGAGGACGACGCCGAGAGGTCACTCGCCCATG 365

QY 132 AGCGAG 137
|||||
Db 364 GCGGAG 359

RESULT 13 711 bp DNA linear GSS 01-OCT-2002
BH925906 B.oleracea002 Brassica oleracea genomic, genomic survey
LOCUS sequence.

ACCESSION BH925906
VERSION BH925906.1 GI:23405972
KEYWORDS GSS.

SOURCE Brassica oleracea

ORGANISM Brassica oleracea

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 711)
Delehaunty,K., Fewell,G., Fulton,L., McCombie,W.R., Miner,T.,
Nash,W., Rabinowicz,P.D. and Wilson,R.K.
Whole genome shotgun reads from Brassica oleracea
Unpublished (2002)

Contact: Richard K. Wilson
Genome Sequencing Center
Washington University School of Medicine
Email: submissions@watson.wustl.edu
Plate: odg84 row: C column: 07
Seq primer: -28RPOT reverse

Class: Shotgun
High quality sequence start: 16
High quality sequence stop: 551.

FEATURES
source Location/Qualifiers

1..711
/organism="Brassica oleracea"
/mol_type="genomic DNA"
/db_xref="taxon:3712"
/clone_lib="B.oleracea002"
/note="Vector: pOTw13; Whole genome shotgun library from
flowering buds. DNA was purified from a crude nuclear
prep using Brassica oleracea TO1000DH3 buds provided by
Thomas Osborn at the University of Wisconsin. Genomic
DNA was provided by Pablo Rabinowicz (CSHL) and the
shotgun library prepared at Washington University Genome
Sequencing Center."

ORIGIN

Query Match 23.6%; Score 36.4; DB 8; Length 711;
Best Local Similarity 55.6%; Pred. No. 34;
Matches 70; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 18 CTCGCTCATCGTCAGTGGCGCGGAGCTGTGTCATCTCGCTCATCGTCGAGTCGCGG 77
|||||

Db 405 CTGCCCCATGGGCGAGGTGACCTCTGCGGGGTCTCTCCGCCCATGCGGCGAGTGACCA 464

Qy 78 CCGCCGACTCGACGATGAGCGAGATGACCAGCTCCGCCGCCGACTCGACGATGACCGAG 137

Db 465 TGGCGGAGGTGACCATGAGGCGAGGTGACCTCGGTGCGGGTCTTCTCTGCTCAGGGCGAG 524

Qy 138 ATGACC 143

Db 525 GTGATC 530

RESULT 14
BH925906/c 711 bp DNA linear GSS 01-OCT-2002
LOCUS odg84c07.g1 B.oleracea002 Brassica oleracea genomic, genomic survey
DEFINITION sequence.
ACCESSION BH925906
VERSION BH925906
KEYWORDS GSS.
SOURCE Brassica oleracea
ORGANISM Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE
1 (bases 1 to 711)
Delehaunty,K., Fewell,G., Fulton,L., McCombie,W.R., Miner,T., Nash,W., Rabinowicz,P.D. and Wilson,R.K.
Whole genome shotgun reads from Brassica oleracea
Unpublished (2002)
Contact: Richard K. Wilson
Genome Sequencing Center
Washington University School of Medicine
Email: submissions@watson.wustl.edu
Plate: odg84 row: C column: 07
Seq primer: -28RPOT reverse
Class: shotgun
High quality sequence start: 16
High quality sequence stop: 551.
Location/Qualifiers
1..711
/organism="Brassica oleracea"
/mol_type="genomic DNA"
/db_xref="taxon:3712"
/clone_lib="B.oleracea002"
/note="Vector: pOTw13; Whole genome shotgun library from flowering buds. DNA was purified from a crude nuclear prep using Brassica oleracea T01000DH3 buds provided by Thomas Osborn at the University of Wisconsin. Genomic DNA was provided by Pablo Rabinowicz (CSHL) and the shotgun library prepared at Washington University Genome Sequencing Center."

ORIGIN

Query Match 23.6%; Score 36.4; DB 8; Length 711;
Best Local Similarity 55.6%; Pred. No. 34;
Matches 70; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

Qy 12 GGTCACTCTGCTCATGTCGAGTCGGCGCGGAGCTGTCATCTCGTCACTCGTAGT 71

Db 530 GATCACTTCGCCCCCTGAGCGAGGAAGACCCGACCGAGGTCACTCGCCCATGTCACT 471

Qy 72 CGGCGCGCGCGACTCGACGATGAGAGATGACCACTCCGCCCGCGACTCGACGATG 131

Db 470 CGCCCATGTGTCACCTCGCCCATGTGGCGAGACGACCCGCGCAGAGTCACTCGCCCATG 411

Qy 132 AGCGAG 137

Db 410 GCGGAG 405

RESULT 15
BZ427562 818 bp DNA linear GSS 13-DEC-2002
LOCUS BZ427562

DEFINITION BONJT45TR BO_1.6_2_KB_tot Brassica oleracea genomic clone BONJT45,
genomic survey sequence.
ACCESSION BZ427562
VERSION BZ427562.1 GI:26669268
KEYWORDS GSS.
SOURCE Brassica oleracea
ORGANISM Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE
1 (bases 1 to 818)
Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.
Whole genome shotgun sequencing of Brassica oleracea
Unpublished (2001)
Other_GSSs: BONJT45TF
Contact: Chris Town
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR
Class: sheared ends.
Location/Qualifiers
1..818
/organism="Brassica oleracea"
/mol_type="genomic DNA"
/strain="T01000DH3"
/db_xref="taxon:3712"
/clone_lib="BONJT45"
/clone_lib="BO_1.6_2_KB_tot"
/note="Vector: pHO51; Site 1: BstXI; 1.6-2 kb sheared total DNA inserted into pHO51 using BstXI linkers"

ORIGIN

Query Match 23.6%; Score 36.4; DB 8; Length 818;
Best Local Similarity 55.6%; Pred. No. 34;
Matches 70; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

Qy 12 GGTCACTCTGCTCATGTCGAGTCGGCGCGGAGCTGTCATCTCGTCACTCGTAGT 71

Db 291 GATCACTTCGCCCCCTGAGCGAGGAAGACCCGACCGAGTCACTCGCCCATGTCACT 350

Qy 72 CGGCGCGCGCGACTCGACGATGAGCGAGATGACCACTCCGCCCGCGACTCGACGATG 131

Db 351 CGCCCATGTGTCACCTCGCCCATGTGGCGAGGAGACGACCCCGCAGAGTCACTCGCCCATG 410

Qy 132 AGCGAG 137

Db 411 GCGGAG 416

RESULT 16
BZ427562 818 bp DNA linear GSS 13-DEC-2002
LOCUS BONJT45TR BO_1.6_2_KB_tot Brassica oleracea genomic clone BONJT45,
genomic survey sequence.
ACCESSION BZ427562
VERSION BZ427562.1 GI:26669268
KEYWORDS GSS.
SOURCE Brassica oleracea
ORGANISM Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE
1 (bases 1 to 818)
Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.
Whole genome shotgun sequencing of Brassica oleracea
Unpublished (2001)
Other_GSSs: BONJT45TF
Contact: Chris Town
TIGR

ORIGIN

Best Local Similarity	55.6%;	Pred. No. 34;
Matches	70; Conservative	56; Indels
		0; Gaps
		0;

Db 416 CTCGCCCATGGGCGAGTACTCTGCGCGGGTCTGCTCTCGGCCCATGGGCGAGGTACCA 357

Db
356 TGGGCGAGTGCATCGGGCGAGTACCTCGGTGCGGCTTTCTCCGCTCAGGGCGAG 297

Db 296 GTGATC 291

DEFINITION OSIFCC045376 *Oryza sativa* Express Library *Oryza sativa* (indica cultivar-group) genomic, genomic survey sequence.

SOURCE ORGANISM
Oryza sativa (indica cultivar-group)
Oryza sativa (indica cultivar-group)

REFERENCE
1 Ehrhartoidae; Oryzae; Oryza.
1 (bases 1 to 834)

its comparison to Arabidopsis
Unpublished (2004)

Rice genomic sequence.
Class: exon-trapped.

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/clone_lib="Oryza sativa Express Library"
/note="Oryza sativa exon trapped genomic sequences"
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ORIGIN

Best Local Similarity	55.6%;	Pred. No. 34;
Matches 70; Conservative	0;	Mismatches 56; Indels 0; Gaps 0;

Db 344 CGGCGCCGCCGCCGCTGGAGTGCCTGGTTCCTCGCGGAGGTGAGGACGGCG 403

Db 404 AGCGGCGGTTCTCTGCCAGGTGCGGCCACGCTTCCAGCCGAGTGCGTCACTGT 463

Db 464 GGCTGC 469

DEFINITION OSIFCC045376 *Oryza sativa* Express Library *Oryza sativa* (indica cultivar-group) genomic, genomic survey sequence.

SOURCE ORGANISM	
Oryza sativa (indica cultivar-group)	
Oryza sativa (indica cultivar-group)	

REFERENCE
1 (bases 1 to 834) Ehrhartoideae; Oryzeae; Oryza.

its comparison to Arabidopsis
Unpublished (2004)

Rice genomic sequence.
Class: exon-trapped.

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/clone_lib="Oryza sativa Express Library"
/note="Oryza sativa exon trapped genomic sequences "
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ORIGIN

Best Local Similarity	55.6%;	Pred. NO. 34;
Matches	70; Conservative	0; Mismatches
		56; Indels
		0; Gaps
		0;

Db 469 GCAGCCACAGTGCAGCCTCGGCGTGGAAAGCCGTGGCCCGCAGCCTTGGGCGACGAACCGCG 410

Db 409 CCGCCTCGCCGTCCTCCACCTCCGCGACACACCGGCACTCCAGCGCGCGCGCGCG 350

Db 349 GCGCCG 344

RESULT 19
CNS030BV
LOCUS
DEFINITION
627 bp DNA linear GSS 01-SEP-2000
Tetraodon nigroviridis genome survey sequence T7 end of clone
041B18 of library G from Tetraodon nigroviridis, genomic survey
sequence.
AL253156
AL253156
GI:7974168
AL253156.1
GSS; genome survey sequence.
Tetraodon nigroviridis
Tetraodon nigroviridis
Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetraodontidae; Tetraodon.
1
REFERENCE
AUTHORS
Roest Crolius,H., Jalllon,O., Dasilva,C., Bouneau,L., Fisher,C.,
Bernot,A., Fizames,C., Winker,P., Brottier,P., Quetier,F.,
Saurin,W. and Weissenbach,J.
Estimate of human gene number provided by genome-wide analysis
using Tetraodon nigroviridis DNA sequence
Nat. Genet. 25 (2), 235-238 (2000)
20296633
JOURNAL
MEDLINE
PUBMED
10835645
2
REFERENCE
AUTHORS
Roest Crolius,H., Jalllon,O., Dasilva,C., Ozouf-Costaz,C.,
Fizames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F.,
Saurin,W., Bernot,A. and Weissenbach,J.
Characterization and repeat analysis of the compact genome of the
freshwater pufferfish Tetraodon nigroviridis
Genome Res. 10 (7), 939-949 (2000)
20359837
JOURNAL
MEDLINE
PUBMED
10899143
3
(bases 1 to 627)
Genoscope.
Direct Submission
Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.
FEATURES
source
1. .627
/organism="Tetraodon nigroviridis"
/mol_type="genomic DNA"
/db_xref="taxon:99883"
/clone="041B18"
/clone_lib="G"
/note="Genoscope sequence ID : C0BG041DA09LP1-end : T7"
ORIGIN
Query Match 23.5%; Score 36.2; DB 9; Length 627;
Best Local Similarity 65.4%; Pred. No. 38;
Matches 53; Conservative 0; Mismatches 28; Indels 0; Gaps 0;
QY 55 CTGCTCATCGTCGAGTCGGCGCCGCGACTCGACGATGAGCGAGATGACCGCTCCG 114
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DB 342 CTCGCTCATGCTCTCGCGCGAGACGCTCTCGACAGCGCGAGACAGACGAGCGCG 401
QY 115 CCGCCGACTCGACGATGAGCG 135
|||||
DB 402 CCGGCTCCCGACATGTCCG 422

RESULT 20
CNS030BV/c
LOCUS
DEFINITION
627 bp DNA linear GSS 01-SEP-2000
Tetraodon nigroviridis genome survey sequence T7 end of clone
041B18 of library G from Tetraodon nigroviridis, genomic survey
sequence.
AL253156
ACCESSION

VERSION
KEYWORDS
SOURCE
ORGANISM
AL253156.1
GI:7974168
GSS; genome survey sequence.
Tetraodon nigroviridis
Tetraodon nigroviridis
Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetraodontidae; Tetraodon.
1
REFERENCE
AUTHORS
Roest Crolius,H., Jalllon,O., Dasilva,C., Bouneau,L., Fisher,C.,
Bernot,A., Fizames,C., Winker,P., Brottier,P., Quetier,F.,
Saurin,W. and Weissenbach,J.
Estimate of human gene number provided by genome-wide analysis
using Tetraodon nigroviridis DNA sequence
Nat. Genet. 25 (2), 235-238 (2000)
20296633
JOURNAL
MEDLINE
PUBMED
10835645
2
REFERENCE
AUTHORS
Roest Crolius,H., Jalllon,O., Dasilva,C., Ozouf-Costaz,C.,
Fizames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F.,
Saurin,W., Bernot,A. and Weissenbach,J.
Characterization and repeat analysis of the compact genome of the
freshwater pufferfish Tetraodon nigroviridis
Genome Res. 10 (7), 939-949 (2000)
20359837
JOURNAL
MEDLINE
PUBMED
10899143
3
(bases 1 to 627)
Genoscope.
Direct Submission
Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.
FEATURES
source
1. .627
/organism="Tetraodon nigroviridis"
/mol_type="genomic DNA"
/db_xref="taxon:99883"
/clone="041B18"
/clone_lib="G"
/note="Genoscope sequence ID : C0BG041DA09LP1-end : T7"
ORIGIN
Query Match 23.5%; Score 36.2; DB 9; Length 627;
Best Local Similarity 68.5%; Pred. No. 38;
Matches 50; Conservative 0; Mismatches 23; Indels 0; Gaps 0;
QY 28 GTGAGTCGCGCGCGAGCTGTCATCTCGCTCATCGATCGAGTCGGCGCCGCGACTC 87
|||||
DB 414 GTCCGGAGCCGCGCGCTCTGTTCTCGCGCTTCGAGACGTCCTCCGCGACGA 355
QY 88 GACGATGAGCGAG 100
|||||
DB 354 GACCATGACGAG 342

RESULT 21
AZ933792
LOCUS
DEFINITION
787 bp DNA linear GSS 24-APR-2001
Bj_Ba001B22f B. japonicum BAC library Bradyrhizobium japonicum
genomic, genomic survey sequence.
AZ933792
AZ933792
GI:13775852
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Bradyrhizobium japonicum
Bradyrhizobium japonicum
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Bradyrhizobiaceae; Bradyrhizobium.
1
(bases 1 to 787)
Tomkins,J.P., Wood,T.C., Stacey,M.G., Loh,J.T., Judd,A.,

Query Match	23.5%;	Score 36.2;	DB 9;	Length 1057;
Best Local Similarity	65.4%;	Pred. No. 38;		
Matches	53;	Conservative	0;	Mismatches 28; Indels 0; Gaps 0;
Qy	55	CTGCTCATCGTCGAGTCGGCGCCGCGACTCGACGATGACGAGATGACGAGCTCCGG	114	
Db	498	CTGCTCATGTCTCTCGTCGGGAGACGTCTCGACAGCGCGAGAACAGCAGAGCGG	557	
Qy	115	CCGCCGACTCGACGATGACG	135	
Db	558	CCGCTCCCGACATGTCCG	578	
RESULT 24				
CNS03W2P/c		1057 bp	DNA	linear
LOCUS				GSS 01-SEP-2000
DEFINITION				Tetraodon nigroviridis genome survey sequence T7 end of clone 063118 of library G from Tetraodon nigroviridis, genomic survey sequence.
ACCESSION		AL263194		GI:7984845
VERSION		AL263194.1		GI:7984845
KEYWORDS		GSS; genome survey sequence.		
SOURCE		Tetraodon nigroviridis		
ORGANISM		Tetraodon nigroviridis		
		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodontidae; Tetraodon.		
REFERENCE		1		
AUTHORS		Roest Crolius,H., Jallion,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizames,C., Wincker,P., Brothier,P., Quettier,F., Saurin,W. and Weissenbach,J.		
TITLE		Estimate of human gene number provided by genome-wide analysis using Tetraodon nigroviridis DNA sequence		
JOURNAL		Nat. Genet. 25 (2), 235-238 (2000)		
MEDLINE		20296633		
PUBMED		10835645		
REFERENCE		2		
AUTHORS		Roest Crolius,H., Jallion,O., Dasilva,C., Ozouf-Costaz,C., Fizames,C., Fischer,C., Bouneau,L., Billault,A., Quettier,F., Saurin,W., Bernot,A. and Weissenbach,J.		
TITLE		Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis		
JOURNAL		Genome Res. 10 (7), 939-949 (2000)		
MEDLINE		20359837		
PUBMED		10899143		
REFERENCE		3		
AUTHORS		(bases 1 to 1057)		
TITLE		Genoscope.		
JOURNAL		Direct Submission		
		Submitted (12-APR-2000) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr		
COMMENT		- Web : www.genoscope.cns.fr)		
		This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at		
		http://www.genoscope.cns.fr/Tetraodon.		
FEATURES				
source		1. 1057		
		/organism="Tetraodon nigroviridis"		
		/mol_type="genomic DNA"		
		/db_xref="taxon:99883"		
		/clone="063118"		
		/clone_lib="G"		
		/note="Genoscope sequence ID : C0BG063BE09LP1-end : T7"		
ORIGIN				
Query Match	23.5%;	Score 36.2;	DB 9;	Length 1057;
Best Local Similarity	68.5%;	Pred. No. 38;		
Matches	50;	Conservative	0;	Mismatches 23; Indels 0; Gaps 0;
Qy	28	GTCGAGTCGGCGCGAGCTGTGATCTCGCTCATCGTGAAGTCGGCGCGCGGACTC	87	

Db	570	GTCGGGAGCCGCGCGCTCTGCTGTCTCGCGCTGTCCGAGACGTCTCCGCGACGA	511	
Qy	88	GACGATGACGCG	100	
Db	510	GACCATGAGCGAG	498	
RESULT 25				
LOCUS		CO435934		
DEFINITION		CO435934		
ACCESSION		CO435934		
VERSION		CO435934.1		
KEYWORDS		EST.		
SOURCE		Oryza sativa (japonica cultivar-group)		
ORGANISM		Oryza sativa (japonica cultivar-group)		
		Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.		
REFERENCE		1		
AUTHORS		Kim,D.S., Lee,I.S., Kang,S.Y., Song,H.S., Lee,Y.I. and Seo,Y.W.		
TITLE		Expressed sequence tag (EST) analysis and characterization of differentially expressed genes related to 5-methyltryptophan (SMT) resistance in mutant rice		
JOURNAL		Unpublished (2003)		
COMMENT		Contact: Seo YM		
		Department of Crop Science, division of Biotechnology and Genetic Engineering		
		Korea University		
		Anam-Dong, Seongbuk-Gu, Seoul, 136-701, Korea		
		Tel: +82 2 3290 3005		
		Fax: +82 2 3290 3501		
		Email: seoag@korea.ac.kr.		
FEATURES				
source		1. 862		
		/organism="Oryza sativa (japonica cultivar-group)"		
		/mol_type="mRNA"		
		/cultivar="Donganbyeon"		
		/db_xref="taxon:39947"		
		/tisue_type="SMT treated leaves, stems, and roots"		
		/dev_stage="seedling grown for 3 weeks"		
		/lab_host="XLI-Blue MRF"		
		/clone_lib="SMT resistant rice mutant cDNA library"		
		/note="Vector: pBluescripts SK(+/-) phagemid; The rice mutant resistant to growth inhibition by SMT were selected from the callus irradiated with gamma ray of 50 Gy through rice cv. Donganbyeon embryo culture. For construction of the cDNA library, SMT resistant homologous rice mutants were treated by SMT for 3 weeks."		
ORIGIN				
Query Match	23.4%;	Score 36;	DB 7;	Length 862;
Best Local Similarity	54.5%;	Pred. No. 43;		
Matches	72;	Conservative	0;	Mismatches 60; Indels 0; Gaps 0;
Qy	18	CTGCTCATCGTCGAGTCGGCGCGCGAGCTGTGATCTCGCTCATCGTCGAGTCGGCGG	77	
Db	139	CTGCTCATGTATGATCATCAGGTGGACCCGGTGTCTCGGCTGGCGCTCTCTCGCGG	198	
Qy	78	CCGCCGACTCGACGATGACGAGATGACCAAGTCCTCCGCGCGCGACTCGACGATGACGAG	137	
Db	199	CCGCCGCGCTCTGCGCACCAAGACGACGGTCTCCGGCTACCGTCCGATCAACATGACG	258	
Qy	138	ATGACCAAGCTCC	149	
Db	259	ACGACCAACACC	270	
RESULT 26				
LOCUS		CO435934		
DEFINITION		OSMR568 SMT resistant rice mutant cDNA library Oryza sativa		

ACCESSION	(japonica cultivar-group) cDNA, mRNA sequence.		
VERSION	CO435934		
KEYWORDS	CO435934.1 GI:53552954		
SOURCE	EST.		
ORGANISM	Oryza sativa (japonica cultivar-group)		
REFERENCE	Oryza sativa (japonica cultivar-group)		
AUTHORS	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
TITLE	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;		
	Ehrhartoideae; Oryzaceae; Oryza.		
	1 (bases 1 to 862)		
	Kim,D.S., Lee,I.S., Kang,S.Y., Song,H.S., Lee,Y.I. and Seo,Y.W.		
	Expressed sequence tag (EST) analysis and characterization of		
	differentially expressed genes related to 5-methyltryptophan (SMT)		
	resistance in mutant rice		
	Unpublished (2003)		
JOURNAL	Contact: Seo YW		
COMMENT	Department of Crop Science, division of Biotechnology and Genetic		
	Engineering		
	Korea University		
	Anam-Dong, Seongbuk-Gu, Seoul, 136-701, Korea		
	Tel: +82 2 3290 3005		
	Fax: +82 2 3290 3501		
	Email: seoag@korea.ac.kr.		
FEATURES	Location/Qualifiers		
source	1..862		
	/organism="Oryza sativa (japonica cultivar-group)"		
	/mol_type="mRNA"		
	/cultivar="Donganbyeon"		
	/db_xref="taxon:39947"		
	/tissue_type="SMT treated leaves, stems, and roots"		
	/dev_stage="seedling grown for 3 weeks"		
	/lab_host="XLI-Blue MRF"		
	/clone_lib="SMT resistant rice mutant cDNA library"		
	/note="Vector: pBluescripts SK(+/-) phagemid; The rice		
	mutant resistant to growth inhibition by SMT were selected		
	from the callus irradiated with gamma ray of 50 Gy.through		
	rice cv. Donganbyeon embryo culture.For construction of the		
	cDNA library, SMT resistant homologous rice mutants were		
	treated by SMT for 3 weeks."		
ORIGIN			
Query Match	23.4%;	Score 36;	DB 7; Length 862;
Best Local Similarity	54.5%;	Pred. No. 43;	
Matches 72; Conservative	0;	Mismatches 60;	Indels 0; Gaps 0;
QY	6	GGAGCTGGTCATCTCGCTCATCTGAGTCGGCGCCGAGCTGTCATCTCGTCATCG	65
Db	270	GGTGCTGTCGTCTGTCATGTCGTCGAGCGGTAGCCGAGACCGTCTTGCGTGGCG	211
QY	66	TCGAGTCGGCGCGCCGAGTCAGTCAGTCGAGCGAGATGACCACTCCGCGCCGACTCG	125
Db	210	AGCGCGCGCGCGCGCGAGAGAGCGCCAGCGAGACCGCGGTGCCACCTGTGATCA	151
QY	126	ACGATGAGCGAG	137
Db	150	TCACGTGATGCAG	139
RESULT 27			
CNS04TDC	972 bp	DNA	linear
LOCUS	GSS 01-SEP-2000		
DEFINITION	Tetraodon nigroviridis genome survey sequence T3 end of clone		
	013112 of library A from Tetraodon nigroviridis, genomic survey		
	sequence.		
ACCESSION	AL306353		
VERSION	AL306353.1 GI:8204690		
KEYWORDS	GSS; genome survey sequence.		
SOURCE	Tetraodon nigroviridis		
ORGANISM	Tetraodon nigroviridis		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;		
	Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;		
	Tetraodontidae; Tetraodontidae; Tetraodon.		

REFERENCE	1
AUTHORS	Roeest Croillius,H., Jalllon,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F., Saurin,W. and Weissenbach,J.
TITLE	Estimate of human gene number provided by genome-wide analysis using Tetraodon nigroviridis DNA sequence
JOURNAL	Nat. Genet. 25 (2), 235-238 (2000)
MEDLINE	20296633
PUBMED	10835645
REFERENCE	2
AUTHORS	Roeest Croillius,H., Jalllon,O., Dasilva,C., Ozouf-Costaz,C., Fizames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and Weissenbach,J.
TITLE	Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
JOURNAL	Genome Res. 10 (7), 939-949 (2000)
MEDLINE	20359837
PUBMED	10899143
REFERENCE	3 (bases 1 to 972)
AUTHORS	Genoscope.
TITLE	Direct Submission
JOURNAL	Submitted (12-APR-2000) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
COMMENT	This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
FEATURES	location/Qualifiers
source	1..972
	/organism="Tetraodon nigroviridis"
	/mol_type="genomic DNA"
	/db_xref="taxon:99883"
	/clone="013112"
	/clone_1lb="A"
ORIGIN	/note="Genoscope sequence ID : C1AA003ZE01A1-end : T3"
Query Match	23.4%; Score 36; DB 9; Length 972;
Best Local Similarity	60.0%; Pred. No. 42;
Matches	57; Conservative 0; Mismatches 38; Indels 0; Gaps 0;
Cy	55 CTCGCTCATCGTCGAGTCGGCGCCGCCGACTCGACGATGAGCGAGATGACCAGCTCCGG 114 474 CTCGCTCATGTGTTCTGTCGGCGGAGGAGCAGTCTCGGACAGCGCCNAGAAGCAGCNAAGCGCG 533
Dn	115 CGCGCCGACTCGACGATGAGCGAGATGACCACTCC 149
Dn	534 CCGGCTCCCGGACATCGTCCGACCCNAGGAACC 568
RESULT 28	
CNS04TDK/c	972 bp DNA linear GSS 01-SEP-2000
LOCUS	Tetraodon nigroviridis genome survey sequence T3 end of clone 01j112 of library A from Tetraodon nigroviridis, genomic survey sequence.
DEFINITION	
ACCESSION	CNS04TDK
VERSION	AL306353 GI:8204690
KEYWORDS	GSS; genome survey sequence.
SOURCE	Tetraodon nigroviridis
ORGANISM	Tetraodon nigroviridis Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes; Tetraodontioidea; Tetraodontidae; Tetraodon.
REFERENCE	1
AUTHORS	Roeest Croillius,H., Jalllon,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F., Saurin,W. and Weissenbach,J.
TITLE	Estimate of human gene number provided by genome-wide analysis using Tetraodon nigroviridis DNA sequence
JOURNAL	Nat. Genet. 25 (2), 235-238 (2000)

MEDLINE 20296633
PUBMED 10835645
REFERENCE 2
AUTHORS Roest Crolius,H., Jailon,O., Dasilva,C., Ozouf-Costaz,C.,
Fizames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F.,
Saurin,W., Bernot,A. and Weissenbach,J.
TITLE Characterization and repeat analysis of the compact genome of the
freshwater pufferfish Tetraodon nigroviridis
JOURNAL Genome Res. 10 (7), 939-949 (2000)
MEDLINE 20359837
PUBMED 10899143
REFERENCE 3 (bases 1 to 972)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : sequef@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.
FEATURES
source
1.972
/organism="Tetraodon nigroviridis"
/mol_type="genomic DNA"
/db_xref="taxon:99883"
/clone="013112"
/clone_lib="A"
/note="Genoscope sequence ID : CIAA003ZE01A1-end : T3"
ORIGIN
Query Match 23.4%; Score 36; DB 9; Length 972;
Best Local Similarity 60.0%; Pred. No. 42;
Matches 57; Conservative 0; Mismatches 38; Indels 0; Gaps 0;
QY 6 GGAGTCGTCATCTCGTCATCTCGAGTCGGCGCCGAGCTGTCATCTCGCTCATCG 65
DB 568 GGTTCCTCTTNGGGTCGACGATGTCGGAGCGCCGCTTGTCTTNGCGCCTGT 509
QY 66 TCGAGTCGGCGCGCCGCGACTCGACGATGAGCGAG 100
DB 508 CCGAGAGTCCTCCGCCGACGAGCATGAGCGAG 474
RESULT 29
BQ767987 367 bp mRNA linear EST 26-JUL-2002
LOCUS EBro08_SQ010_K07_R root, 3 week, drought-stressed, cv Optic, EBro08
DEFINITION Hordeum vulgare subsp. vulgare cDNA clone EBro08_SQ010_K07 5', mRNA
sequence.
ACCESSION BQ767987
VERSION BQ767987
KEYWORDS BQ767987.1 GI:21976461
SOURCE EST.
ORGANISM Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Hordeum.
REFERENCE 1 (bases 1 to 367)
AUTHORS Hedley,P., Liu,H., Caldwell,D., McCallum,N., Mudie,S., Cardle,L.,
Ramsay,L., Machray,G., Marshall,D.F.M. and Waugh,R.
TITLE Development of Barley Transcriptome Resources
JOURNAL Unpublished (2001)
COMMENT Contact: Waugh R, Marshall DF
Genome Dynamics/Computational Biology
Scottish Crop Research Institute
Invergowrie, Dundee, DD2 5DA, Scotland, UK
Tel: 00 44 1382 562731
Fax: 00 44 1382 562426
Email: est@scri.sari.ac.uk.
location/Qualifiers
1.367
FEATURES
source
/organism="Hordeum vulgare subsp. vulgare"

/mol_type="mRNA"
/cultivar="Optic"
/sub_species="vulgare"
/db_xref="taxon:112509"
/clone="EBro08_SQ010_K07"
/tissue_type="root"
/dev_stage="3 week"
/lab_host="DH10B"
/clone_lib="root, 3 week, drought-stressed, cv Optic,
EBro08"
/note="Vector: pSPORT1; Site_1: Sal I; Site_2: Not I;
Non-normalised library, directionally cloned into pSPORT1.
Derived from roots of 3 week old drought stressed barley
plants. Developed as part of the barley transcriptome
resources of BBSRC/SEERAD funded cereal IGF (Investigating
Gene Function) project."
ORIGIN
Query Match 23.2%; Score 35.8; DB 5; Length 367;
Best Local Similarity 55.1%; Pred. No. 49;
Matches 70; Conservative 0; Mismatches 57; Indels 0; Gaps 0;
QY 1 CGGCCGAGCTGTGTCATCTCGTCATCTCGAGTCGGCGCCGAGCTGTGTCATCTCGCT 60
DB 220 CGGCACGACCGCGCGCAGCAGCACCAGCCAGCTGCCCGCAGCTCACTCGACCT 279
QY 61 CATGTCGAGTCGGCGCGCCCGCACTCGACGATGAGCGAGATGACCACTCGCGCGCG 120
DB 280 GTCCGTGGCGCCCGCGCGCGCAGCAGCGCCGAGCTGCAACCCGGTCTGCTTGCCTGCGCCA 339
QY 121 ACTCGAC 127
DB 340 CCTCGGC 346
RESULT 30
BQ767987/c 367 bp mRNA linear EST 26-JUL-2002
LOCUS EBro08_SQ010_K07_R root, 3 week, drought-stressed, cv Optic, EBro08
DEFINITION Hordeum vulgare subsp. vulgare cDNA clone EBro08_SQ010_K07 5', mRNA
sequence.
ACCESSION BQ767987
VERSION BQ767987
KEYWORDS BQ767987.1 GI:21976461
SOURCE EST.
ORGANISM Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Hordeum.
REFERENCE 1 (bases 1 to 367)
AUTHORS Hedley,P., Liu,H., Caldwell,D., McCallum,N., Mudie,S., Cardle,L.,
Ramsay,L., Machray,G., Marshall,D.F.M. and Waugh,R.
TITLE Development of Barley Transcriptome Resources
JOURNAL Unpublished (2001)
COMMENT Contact: Waugh R, Marshall DF
Genome Dynamics/Computational Biology
Scottish Crop Research Institute
Invergowrie, Dundee, DD2 5DA, Scotland, UK
Tel: 00 44 1382 562731
Fax: 00 44 1382 562426
Email: est@scri.sari.ac.uk.
location/Qualifiers
1.367
FEATURES
source
/organism="Hordeum vulgare subsp. vulgare"
/mol_type="mRNA"
/cultivar="Optic"
/sub_species="vulgare"
/db_xref="taxon:112509"
/clone="EBro08_SQ010_K07"
/tissue_type="root"
/dev_stage="3 week"
/lab_host="DH10B"
/clone_lib="root, 3 week, drought-stressed, cv Optic,

SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 624)
Jantasuriyarat,C., Lu,G., Gowda,M., Hatfield,J., Zhou,B., Mazur,E.,
Kudrna,D., Dean,R., Soderlund,C., Wing,R. and Wang,G.
Large-scale identification of ESTs involved in the interaction
between rice and Magnaporthe grisea
Unpublished (2003)
JOURNAL Contact: Rod Wing
COMMENT Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
85721-0088, USA
Tel: 520 626 3967
Fax: 520 621 9288
Email: http://genome.arizona.edu
PCR Primers
FORWARD: gta aaa cga cgg cca gtcg
BACKWARD: gga aac agc tat gac cat g
Plate: 09 row: L column: 11
Seq primer: gta aaa cga cgg cca gtcg.
Location/Qualifiers
1. .624
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="OSJNEf09L11"
/tissue_type="Leaf"
/dev_stage="3 week"
/lab_host="DH108"
/clone_lib="OSJNEf"
/note="Vector: pBluescript II KS +; Site_1: EcoRI; Site_2:
XhoI; Uninfected Control"
ORIGIN
Query Match 23.1%; Score 35.6; DB 6; Length 624;
Best Local Similarity 60.2%; Pred. No. 54;
Matches 59; Conservative 0; Mismatches 39; Indels 0; Gaps 0;
Oy 21 GCTCATGTCGAGTCGGCGCGCGGAGCTGTCATCTGTCATCTGAGTCGGCGCGG 80
Db 287 GGTCTCGGAGCGGATGCAGCGCGGTGCGGCTCAACCCGGTGTGGCCGCGCGCGCGG 346
Oy 81 CCGACTCGACGATGAGCGAGATGACCACTCCGCGCGC 118
Db 347 CCGTCTCGGCGTCCACCAAGAAGTGCTCCCGCGGAGC 384
RESULT 34
CB682412/c 624 bp mRNA linear EST 09-APR-2003
LOCUS OSJNEf09L11.f OSJNEf Oryza sativa (japonica cultivar-group) cDNA
DEFINITION clone OSJNEf09L11 5', mRNA sequence.
ACCESSION CB682412
VERSION CB682412
KEYWORDS
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 624)
Jantasuriyarat,C., Lu,G., Gowda,M., Hatfield,J., Zhou,B., Mazur,E.,
Kudrna,D., Dean,R., Soderlund,C., Wing,R. and Wang,G.
Large-scale identification of ESTs involved in the interaction
between rice and Magnaporthe grisea
Unpublished (2003)
JOURNAL Contact: Rod Wing
COMMENT Arizona Genomics Institute

University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
85721-0088, USA
Tel: 520 626 3967
Fax: 520 621 9288
Email: http://genome.arizona.edu
PCR Primers
FORWARD: gta aaa cga cgg cca gtcg
BACKWARD: gga aac agc tat gac cat g
Plate: 09 row: L column: 11
Seq primer: gta aaa cga cgg cca gtcg.
Location/Qualifiers
1. .624
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="OSJNEf09L11"
/tissue_type="Leaf"
/dev_stage="3 week"
/lab_host="DH108"
/clone_lib="OSJNEf"
/note="Vector: pBluescript II KS +; Site_1: EcoRI; Site_2:
XhoI; Uninfected Control"
ORIGIN
Query Match 23.1%; Score 35.6; DB 6; Length 624;
Best Local Similarity 58.5%; Pred. No. 54;
Matches 62; Conservative 0; Mismatches 44; Indels 0; Gaps 0;
Oy 37 GCGGCGGAGCTGTGTCATCTCGTCTCATCTGTCGAGTCGGCGCGCGGCGGACTGCAGATGAG 96
Db 384 GCTCCCGGAGACCACTTCTTGTTGTCAGCGCCGAGACGCGCGCGCGCGGCCACAC 325
Oy 97 CGAGATGACCACTCCGCGCGCGGCACTGCAGCATGACGAGATGAC 142
Db 324 CGGTTGAGCCGACCGCCTGCATCCGCTCCGACGACCCCGCGGC 279
RESULT 35
CA198784 677 bp mRNA linear EST 25-SEP-2003
LOCUS SCCST3C12B03.g ST3 Saccharum officinarum cDNA clone SCCST3C12B03
DEFINITION 5', mRNA sequence.
ACCESSION CA198784
VERSION CA198784.1 GI:35230393
KEYWORDS
SOURCE Saccharum officinarum
ORGANISM Saccharum officinarum
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum
complex.
1 (bases 1 to 677)
Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.
The libraries that made SUCEST
Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
Contact: Arruda P
Centro de Biologia Molecular e Engenharia Genetica
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
Email: parruda@unicamp.br
Clone distribution: clone distribution information can be found
through the Brazilian Clone Collection Center (BCCC) at
http://www.bcccenter.fcav.unesp.br
Plate: C12 row: B column: 03
Seq primer: T7 Promoter Primer.
Location/Qualifiers
1. .677
/organism="Saccharum officinarum"
/mol_type="mRNA"

/db_xref="taxon:4547"
/clone="SCCST3C12B03"
/lab_host="DH10B"
/clone_lib="ST3"
/note="Origin: Fourth apical stalk internodes of adult plants; Vector: pSport1, Site 1: SalI; Site 2: NotI; An unidirectional cDNA library generated from [Fourth apical stalk internodes of adult plants]. cDNA was prepared from polyA+ mRNA using Superscript Plasmid System Kit (Invitrogen). The double-strand cDNAs were fractionated in a sepharose CL-2B 40cm-columns and fragments sizing between 0.8 and 1.5 Kb were directionally cloned into the vector. Details of each source of RNA and library construction can be obtained at
<http://sucest.lad.ic.unicamp.br/public>"

ORIGIN

Query Match 23.1%; Score 35.6; DB 6; Length 677;
Best Local Similarity 58.8%; Pred. No. 54;
Matches 80; Conservative 0; Mismatches 54; Indels 2; Gaps 1;

QY 9 GCTGTCATCTCGTCATCTGTCGA--GTCGCGCGCCGAGCTGTCATCTCGTCATCTG 66
Db 439 GCTGATCGCCGCGCTCATCGACGACGCGCGCGAAGACCAAGCCATCGCCGTCACATG 498
QY 67 CGAGTCGCGCGCGCGCGCTGACGATGAGAGATGACCACTCCGCGCGCGCATCTGA 126
Db 499 CGAGGTGTGCTGTTGACCACTGCTGTGATGCTGACACGCGCGTGCACCTCCACGA 558
QY 127 CGATGAGCGAGATGAC 142
Db 559 CGAGGCGGACGACGAC 574

RESULT 36
CA198784/c
LOCUS CA198784 677 bp mRNA linear EST 25-SEP-2003
DEFINITION SCCST3C12B03.g ST3 Saccharum officinarum cDNA clone SCCST3C12B03
5', mRNA sequence.

ACCESSION CA198784
VERSION CA198784
KEYWORDS GI:35230393
SOURCE EST.

ORGANISM Saccharum officinarum
Saccharum officinarum

REFERENCE
AUTHORS Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.
TITLE The libraries that made SUCEST
JOURNAL Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
COMMENT Contact: Arruda P
Centro de Biologia Molecular e Engenharia Genetica
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
Email: parnuda@unicamp.br
Clone distribution: clone collection information can be found
<http://www.bcccenter.fcav.unesp.br>
through the Brazilian Clone Collection Center (BCCC) at
plate: C12 row: B column: 03
Seq primer: T7 Promoter Primer.

REFERENCE
AUTHORS Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.
TITLE The libraries that made SUCEST
JOURNAL Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
COMMENT Contact: Arruda P
Centro de Biologia Molecular e Engenharia Genetica
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
Email: parnuda@unicamp.br
Clone distribution: clone collection information can be found
<http://www.bcccenter.fcav.unesp.br>
through the Brazilian Clone Collection Center (BCCC) at
plate: C12 row: B column: 03
Seq primer: T7 Promoter Primer.

FEATURES
source location/Qualifiers
1..677

/organism="Saccharum officinarum"
/mol_type="mRNA"
/db_xref="taxon:4547"
/clone="SCCST3C12B03"
/lab_host="DH10B"
/clone_lib="ST3"
/note="Organ: Fourth apical stalk internodes of adult

plants; Vector: pSport1, Site 1: SalI; Site 2: NotI; An unidirectional cDNA library generated from [Fourth apical stalk internodes of adult plants]. cDNA was prepared from polyA+ mRNA using Superscript Plasmid System Kit (Invitrogen). The double-strand cDNAs were fractionated in a sepharose CL-2B 40cm-columns and fragments sizing between 0.8 and 1.5 Kb were directionally cloned into the vector. Details of each source of RNA and library construction can be obtained at
<http://sucest.lad.ic.unicamp.br/public>"

ORIGIN

Query Match 23.1%; Score 35.6; DB 6; Length 677;
Best Local Similarity 58.8%; Pred. No. 54;
Matches 80; Conservative 0; Mismatches 54; Indels 2; Gaps 1;

QY 13 GTCATCTGCTCATCTGAGTCGCGCGCGAGCTGTCATCTCGTCATCTCGAGTC 72
Db 574 GTGTCGTCGCCCTCGTCGAGAGTCGACGCGCTGTCACGATCCACAGAGTGTC 515
QY 73 GCGCGCGCGCGCTGACGATGAGCGAGATGACCACTCCGCGCGCGAC--TCGACGAT 130
Db 514 GACACAGACCACTCGCAGTTGACGCGGATGGGCTGTCTTCCGCCCGCGTCTGAT 455
QY 131 GAGCGAGATGACGACG 146
Db 454 GAGCGCGCGATCAGC 439

RESULT 37
AI399069
LOCUS AI399069 590 bp mRNA linear EST 08-FEB-1999
DEFINITION NCW01B1173 Westergaards Neurospora crassa cDNA clone W01B11 5',
mRNA sequence.

ACCESSION AI399069
VERSION AI399069
KEYWORDS GI:4242154
SOURCE EST.

ORGANISM Neurospora crassa
Neurospora crassa

REFERENCE
AUTHORS Nelson,M.A., Kang,S., Braun,E.L., Crawford,M.E., Dolan,P.L.,
Leonard,P.M., Mitchell,J., Armijo,A.M., Bean,L., Blueyes,E.,
Cushing,T., Errett,A., Fleharty,M., Gorman,M., Judson,K.,
Miller,R., Ortega,J., Pavlova,I., Perea,J., Todisco,S.,
Trujillo,R., Valentine,J., Wells,A., Werner-Washburne,M., Yazzie,S.
and Natvig,D.O.
Expressed sequences from conidial, mycelial, and sexual stages of
Neurospora crassa
Fungal Genet. Biol. 21, 348-363 (1997)
9290248

COMMENT Contact: Natvig,D.O./Nelson,M.A.
Department of Biology
University of New Mexico
Cascabel Hall, Albuquerque, NM 87131, USA
Tel: 505 277 3411
Fax: 505 277 0304
Email: ngp@biology.unm.edu.
location/Qualifiers
1..590

FEATURES
source location/Qualifiers
1..590

/organism="Neurospora crassa"
/mol_type="mRNA"
/strain="74-OR23-IV A (FGSC 2489)"
/db_xref="taxon:5141"
/clone="W01B11"
/sex="Mating type A"
/tissue_type="Unfertilized sexual tissue"
/dev_stage="Unfertilized sexual stage"
/lab_host="E. coli"
/clone_lib="Westergaards"
/note="Vector: pBluescript SK (-); Site_1: EcoRI; Site_2:

XhoI; Westergaard's medium (Nitrogen limiting). Floating mycelial mats grown at 25C for 36 hours. cDNA directionally cloned into pBluescript SK(-) using the Uni-ZAP XR vector system (Stratagene, La Jolla, CA)."

Query Match 23.0%; Score 35.4; DB 1; Length 590; Best Local Similarity 57.3%; Pred. No. 61; Matches 63; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

Oy 18 CTCGCTCATCGTCGAGTCGGCGCGCGAGCTGTCATCTCGCTCATCGTCGAGTCGGCGG 77
Db 81 CTCGCTCATCGCCAGAGCCCGCGCCACACAGCCTCTCGCTCGTCTCCAGGCGCGCCG 140
Oy 78 CCGCCGACTCGACGATGAGCGAGATGACCGCTCCGCGCGCGACTCGAC 127
Db 141 CCGCGTTACCAATACCACTGCTACTCAGCCCCCAGCCGACAGTGCC 190

RESULT 38 AI399069 590 bp mRNA linear EST 08-FEB-1999
LOCUS AI399069/c NCM01B113 Westergaards Neurospora crassa cDNA clone W01B1 5',
DEFINITION mRNA sequence.

ACCESSION AI399069 GI:4242154
VERSION AI399069.1
KEYWORDS EST.
SOURCE Neurospora crassa
ORGANISM Neurospora crassa
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
REFERENCE 1 (bases 1 to 590)
AUTHORS Nelson,M.A., Kang,S., Braun,E.L., Crawford,M.E., Dolan,P.L., Leonard,P.M., Mitchell,J., Armijo,A.M., Bean,L., Blueyes,E., Cushing,T., Eretert,A., Fleharty,M., Gorman,M., Judson,K., Miller,R., Ortega,J., Pavlova,I., Perea,J., Todisco,S., Trujillo,R., Valentine,J., Wells,A., Werner-Washburne,M., Yazzie,S. and Natvig,D.O.
Expressed sequences from conidial, mycelial, and sexual stages of Neurospora crassa
Fungal Genet. Biol. 21, 348-363 (1997)

TITLE
JOURNAL MEDLINE
PUBMED 9290248
COMMENT Contact: Natvig,D.O./Nelson,M.A.
Department of Biology
University of New Mexico
Casteretter Hall, Albuquerque, NM 87131, USA
Tel: 505 277 3411
Fax: 505 277 0304
Email: ngp@biology.unm.edu.

FEATURES
source 1. 590
/organism="Neurospora crassa"
/mol_type="mRNA"
/strain="74-OR23-IV A (FGSC 2489)"
/db_xref="taxon:5141"
/clone="W01B11"
/sex="Mating type A"
/tissue_type="Unfertilized sexual tissue"
/dev_stage="Unfertilized sexual stage"
/lab_host="E. coli"
/clone_lib="Westergaards"
/note="Vector: pBluescript SK (-); Site_1: EcoRI; Site_2: XhoI; Westergaard's medium (Nitrogen limiting). Floating mycelial mats grown at 25C for 36 hours. cDNA directionally cloned into pBluescript SK(-) using the Uni-ZAP XR vector system (Stratagene, La Jolla, CA)."

ORIGIN
Query Match 23.0%; Score 35.4; DB 1; Length 590;
Best Local Similarity 57.3%; Pred. No. 61;
Matches 63; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

Oy 28 GTGAGTCGGCGCGCGAGCTGTCATCTCGTCATCGTCAGTCGGCGCGCGACTC 87
Db 190 GGCCACTGTCCGGCTGGGGGTGAGTATGAGACTGTANTGTAAACCGCGCGCGCCCT 131
Oy 88 GACGATGACCGAGATGACCACTCCGCGCGCGACTCGACGATGAGCGAG 137
Db 130 GGAGACGAGCGAGGAGGCTTTGGCGCGCGGCTTCTGGCGGATGAGCGAG 81

RESULT 39 CA227997 704 bp mRNA linear EST 25-SBP-2003
LOCUS SCJLFL3015B05.b Saccharum officinarum FL3 Saccharum officinarum
DEFINITION cDNA clone SCJLFL3015B05 3', mRNA sequence.

ACCESSION CA227997 GI:35289071
VERSION CA227997.1
KEYWORDS EST.
SOURCE Saccharum officinarum
ORGANISM Saccharum officinarum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum complex.

REFERENCE 1 (bases 1 to 704)
AUTHORS Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.
TITLE The libraries that made SUCEST
JOURNAL Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
COMMENT Contact: Arruda P
Centro de Biologia Molecular e Engenharia Genetica
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
Email: parruda@unicamp.br
Clone distribution: clone distribution information can be found through the Brazilian Clone Collection Center (BCCC) at http://www.bcccenter.fcav.unesp.br
Plate: 015 row: B column: 05
Seq primer: SP6 Promoter primer.

FEATURES
source 1. 704
/organism="Saccharum officinarum"
/mol_type="mRNA"
/db_xref="taxon:4547"
/clone="SCJLFL3015B05"
/lab_host="DH10B"
/clone_lib="Saccharum officinarum FL3"
/note="Organ: Base of developing inflorescence (5cm-long); Vector: pSport1; Site_1: SalI; Site_2: NotI; An unidirectional cDNA library generated from [Base of developing inflorescence (5cm-long)]. cDNA was prepared from polyA+ mRNA using Superscript Plasmid System Kit (Invitrogen). The double-strand cDNAs were fractionated in a sepharose CL-2B 40cm-columns and fragments sizing between 0.8 and 1.5 Kb were directionally cloned into the vector. Details of each source of RNA and library construction can be obtained at http://sucest.lad.ic.unicamp.br/public"

ORIGIN
Query Match 23.0%; Score 35.4; DB 6; Length 704;
Best Local Similarity 52.3%; Pred. No. 61;
Matches 78; Conservative 0; Mismatches 71; Indels 0; Gaps 0;

Oy 2 GGCCGAGCTGTGTCATCTCGCTCATCGTCGAGTCGGCGCGGAGCTGTCTCGCTC 61
Db 264 GGCTCTCTCTGAGGCTGAGGCCCGCGAGCGGGGGCTGGCACGCTGTCTCTCACC 323
Oy 62 ATCGTCAGTCGGCGCGCGCACTCGACGATGACGAGATGACCACTCGCGCGCGGA 121
Db 324 GCCGACCAAGCAGGGGCTCTTACAAAGTCGAGCGAGATGTCCATCTCGCGACCTC 383
Oy 122 CTCGACGATGAGCGAGATGACCACTCGC 150

SOURCE ORGANISM	REFERENCE AUTHORS	TITLE	JOURNAL COMMENT	FEATURES source
Triticum aestivum (bread wheat)				
Triticum aestivum				
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae; Triticeae; Triticum.				
1 (bases 1 to 441)				
Anderson, O.D., Chao, S., Choi, D.W., Close, T.J., Fenton, R.D., Han, P.S., Hsia, C.C., Kang, Y., Lazo, G.R., Miller, R., Rausch, C.J., Seaton, C.L. and Tong, J.C.				
The structure and function of the expressed portion of the wheat genomes - Pre-anthesis spike cDNA library				
Unpublished (2000)				
Contact: Olin Anderson				
US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center				
800 Buchanan Street, Albany, CA 94710, USA				
Tel: 5105595773				
Fax: 5105595818				
Email: oandersn@pw.usda.gov				
Sequence have been trimmed to remove vector sequence and low quality sequence with phred score less than 20				
Seq primer: Stratagene SK primer.				
Location/Qualifiers				
1..441				
/organism="Triticum aestivum"				
/mol_type="mRNA"				
/cultivar="Chinese Spring"				
/db_xref="taxon:4565"				
/clone="WHE2314 D05 G10"				
/tissue_type="Spike before anthesis"				
/dev_stage="Adult plant"				
/lab_host="E. coli SOLR"				
/clone_lib="wheat pre-anthesis spike cDNA library"				
/note="Vector: Lambda Uni-ZAP XR, excised phagemid; Site_1: EcoRI; Site_2: XhoI; Plants were grown in the greenhouse. Whole spike with awns trimmed, white, green and yellow anther were collected and total RNA, and poly(A) RNA were prepared, a cDNA library was made, and the cDNA clones were in vivo excised to give Bluescript phagemids in the T7 Close lab (Choi, Close, Fenton) at the University of California, Riverside. Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."				
ORIGIN				
Query Match	22.7%	Score 35;	DB 2;	Length 441;
Best Local Similarity	63.9%	Pred. No. 78;		
Matches	53;	Conservative	0;	Mismatches 30; Indels 0; Gaps 0;
QY	46	GCTGTCATCTCGCTCATGTCGAGTCGGCGCCGCCGACTCGACGATGAGCGAGATGAC	105	
Db	102	GCCGTTGCCGTCGCCCTTGCGCCGAAGCCGCGGACGCCGCCGCGAGAGAGAGAGAGAG	43	
QY	106	CAGCTCCGGCGCCCGGACTGACG	128	
Db	42	GACGCGCGCGCGCCGCTCGACG	20	
RESULT 43				
LOCUS	BQ805125	571 bp	mRNA	linear EST 31-JUL-2002
DEFINITION	WHE3563_B09_C17S wheat developing grains cDNA library Triticum aestivum cDNA clone WHE3563_B09_C17, mRNA sequence.			
ACCESSION	BQ805125			
VERSION	BQ805125.1	GI:22029334		
KEYWORDS	EST.			
SOURCE	Triticum aestivum (bread wheat)			
ORGANISM	Triticum aestivum			
REFERENCE	Altanbach, S., Anderson, O.D., Chao, S., Chin, A., Close, T.J.,			

Cronin,K., Crossman,C., Fenton,R.D., Lazo,G.R., Pham,J., Rausch,C.J., Wilson,C. and Woo,J.
The structure and function of the expressed portion of the wheat genomes - Developing grains cdna library
Unpublished (2002)
Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
Fax: 5105595818
Email: oanderson@pw.usda.gov
Sequences have been trimmed to remove vector sequence and low quality sequence with phred score less than 20
Seq primer: SK primer.

JOURNAL COMMENT

TITLE

FEATURES

source

1..571
/organism="Triticum aestivum"
/mol_type="mRNA"
/cultivar="Butte 86"
/db_xref="taxon:4565"
/clone="WHE3563 B09 C17"
/tissue_type="whole grains"
/dev_stage="3-44 days post anthesis seed"
/lab_host="E. coli SOLR"
/clone_lib="wheat developing grains cdna library"
/note="Vector: Lambda ZAP II, excised phagmid; Site 1:
ECORI; Plants were grown under six following different environmental regimes in greenhouse, Environment 1) 24OC/17OC day/night, well-watered, with post-anthesis fertilizer, Environment 2) 24OC/17OC day/night, well-watered, without post-anthesis fertilizer,
Environment 3) 37OC/17OC day/night, well-watered, with post-anthesis fertilizer, Environment 4) 37OC/17OC day/night, well-watered, without post-anthesis fertilizer, Environment 5) 37OC/17OC day/night plus drought, with post-anthesis fertilizer, Environment 6) 37OC/17OC day/night plus drought, without post-anthesis fertilizer, developing wheat grains from the following were excised and frozen in liquid nitrogen, Environment 1 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 32, 36, 40, 44 DPA Environment 2 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 32, 36, 40, 44 DPA Environment 3 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 32, 34 DPA Environment 4 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 32, 34 DPA Environment 5 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 30 DPA Environment 6 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 30 DPA and total RNA was prepared by S. Altenbach and K. Cronin at USDA-ARS, Albany, CA. A cDNA library was made using poly (A) RNA, and the cDNA clones were in vivo excised to give pluescript SK(-) phagemids in the T7 Close lab (Chin, Close, Fenton) at the University of California, Riverside. Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (others)."

ORIGIN:

Query Match 22.7%; Score 35; DB 5; Length 571;
Best Local Similarity 63.9%; Pred. No. 77;
Matches 53; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

OY 27 CGTCGAGTCGGCGCCGAGAGCTGTATCTCGCTCATGCTGAGTCGGCGGCCGCACT 86
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 116 CGTCGAGCGCGCGCCGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 175
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 87 CGACGATGAGCGAGATGACCAGC 109
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 176 CGGCCAGGCGGCACGCAACGCGC 198

RESULT 44
BQ805125/c 571 bp mRNA linear EST 31-JUL-2002
DEFINITION WHE3563_B09 C17ZS Wheat developing grains cdna library Triticum

accession cdna clone WHE3563_B09_C17, mRNA sequence.
BQ805125
VERSION BQ805125.1 GI:22029334
KEYWORDS EST.
SOURCE Triticum aestivum (bread wheat)
ORGANISM Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Triticum.
1 (bases 1 to 571)
REFERENCE Altenbach,S., Anderson,O.D., Chao,S., Chin,A., Close,T.J.,
Cronin,K., Crossman,C., Fenton,R.D., Lazo,G.R., Pham,J.,
Rausch,C.J., Wilson,C. and Woo,J.
The structure and function of the expressed portion of the wheat
genomes - Developing grains cdna library
JOURNAL Unpublished (2002)
COMMENT Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
Fax: 5105595818
Email: oandersn@pw.usda.gov
Sequences have been trimmed to remove vector sequence and low
quality sequence with phred score less than 20
Seq primer: SK primer.
FEATURES
source
1..571
/organism="Triticum aestivum"
/mol_type="mRNA"
/cultivar="Butte 86"
/db_xref="taxon:4565"
/clone="WHE3563_B09_C17"
/tissue_type="whole grains"
/dev_stage="3-44 days post anthesis seed"
/lab_host="E. coli SOLR"
/clone_lib="Wheat developing grains cdna library"
/note="Vector: Lambda ZAP II, excised phagemid: Site 1:
ECORI; Plants were grown under six following different
environmental regimes in greenhouse, Environment 1)
240C/170C day/night, well-watered, with post-anthesis
fertilizer, Environment 2) 240C/170C day/night,
well-watered, without post-anthesis fertilizer,
Environment 3) 370C/170C day/night, well-watered, with
post-anthesis fertilizer, Environment 4) 370C/170C
day/night, well-watered, without post-anthesis fertilizer,
Environment 5) 370C/170C day/night plus drought, with
post-anthesis fertilizer, Environment 6) 370C/170C
day/night plus drought, without post-anthesis fertilizer,
developing wheat grains from the following were excised
and frozen in liquid nitrogen, Environment 1 at 3, 5, 7,
8, 10, 12, 16, 20, 24, 28, 32, 36, 40, 44 DPA Environment
2 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 32, 36, 40, 44
DPA Environment 3 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28,
32, 34 DPA Environment 4 at 3, 5, 7, 8, 10, 12, 16, 20,
24, 28, 32, 34 DPA Environment 5 at 3, 5, 7, 8, 10, 12,
16, 20, 24, 28, 30 DPA Environment 6 at 3, 5, 7, 8, 10,
12, 16, 20, 24, 28, 30 DPA and total RNA was prepared by
S. Altenbach and K. Cronin at USDA-ARS, Albany, CA. A
cdna library was made using poly (A) RNA, and the cdna
clones were in vivo excised to give pBluescript SK(-)
phagemids in the TU Close lab (Chin, Close, Fenton) at
the University of California, Riverside. Plasmid DNA
preparations and DNA sequencing were performed in the OD
Anderson lab (others)."

ORIGIN

Query Match 22.7%; Score 35; DB 5; Length 571;
Best Local Similarity 63.9%; Pred. No. 77;
Matches 53; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 46 GCTGTCATCTCGCTCATCTGTCGAGTGGCGCGCCGCGACTCGACGATGAGCGAGATGAC 105
|||||

Db 198 GCCGTTGCCGTGCCCCCTGGCCGGAAGCCGCGGACGCCCGCGAGAGAGAGAGAG 139
QY 106 CAGTCCGCGCGCGCGACTGACG 128
Db 138 GACGCGCGCGCGCGCGCTGACG 116

RESULT 45
BG279219
LOCUS BG279219
DEFINITION bf104np.r1 Neurospora crassa sexual cdna library, Uni-zap vector
system Neurospora crassa cdna clone bf104np 5', mRNA sequence.
ACCESSION BG279219
VERSION BG279219.1 GI:13076367
KEYWORDS EST.
SOURCE Neurospora crassa
ORGANISM Neurospora crassa
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
1 (bases 1 to 430)
REFERENCE Kupfer,D., Lai,H., Nelson,M. and Roe,B.
ESTs from a Neurospora crassa Sexual cdna library
JOURNAL Unpublished (2001)
COMMENT Other ESTs: bf104np.fl
Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
Department of Chemistry and Biochemistry
Advanced Center for Genome Technology, University of Oklahoma
620 Parrington Oval, Norman, OK 73019, USA
Tel: 405 325 4912
Fax: 405 325 7762
Email: broe@ou.edu
Contact Dr. Mary Anne Nelson, Department of Biology, University of
New Mexico, Albuquerque, NM 87131 (e-mail address manelson@unm.edu)
regarding clone availability
Seq primer: M13 Universal Reverse Primer
High quality sequence stop: 419.

FEATURES

source
1..430
/organism="Neurospora crassa"
/mol_type="mRNA"
/strain="wild type"
/db_xref="taxon:5141"
/clone="bf104np"
/tissue_type="perithecia (fruiting bodies)"
/dev_stage="sexual"
/lab_host="E. coli strain SOLR"
/clone_lib="Neurospora crassa sexual cdna library, Uni-zap
vector system"
/note="Vector: pBluescript SK-; Site 1: EcorI; Site_2:
XhoI; 5' end of cdna cloned into EcorI site of
pBluescript; 3' end of cdna cloned into XhoI site of
pBluescript"

ORIGIN

Query Match 22.6%; Score 34.8; DB 4; Length 430;
Best Local Similarity 57.3%; Pred. No. 87;
Matches 63; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

QY 18 CTCGTCATCTGTCGATGTCGCGCGCGAGCTGTCATCTGCTCATCTGTCGTCGCGG 77
Db 229 CTCGTCATCTGTCGAGAGCGCGCGCCAGACAGCTTCCTGCTGTCGTCGAGCGCGG 288
QY 78 CCGCGACTCGACGATGAGGAGATGACCAAGCTCCGCGCGCGGACTGAC 127
Db 289 CCGCGGTAACAGTACGATCTACTAGCCCCAGCGGACAGTGGCC 338

Search completed: April 9, 2005, 00:50:56
Job time : 3133 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 8, 2005, 23:20:25 ; Search time 504 Seconds
(without alignments)
1851.668 Million cell updates/sec

Title: US-09-887-194A-13

Perfect score: 154

Sequence: 1 cggccgagctggtcatctc.....gagatgaccagctccgcg 154

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 5615251 seqs, 3030001701 residues

Total number of hits satisfying chosen parameters: 11230502

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Published Applications NA:*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
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- 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
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- 14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
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- 17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
- 18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:*
- 19: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 20: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
- 21: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 22: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	154	100.0	154	10	US-09-887-194A-13
2	154	100.0	154	10	US-09-887-194A-13
3	154	100.0	154	10	US-09-934-900-25
4	154	100.0	154	10	US-09-934-900-25
5	154	100.0	154	18	US-10-734-947-7
6	154	100.0	154	18	US-10-734-947-7
7	154	100.0	154	19	US-10-981-293-25
8	154	100.0	154	19	US-10-981-293-25
9	154	100.0	7701	17	US-10-459-159-1
10	154	100.0	7701	17	US-10-459-159-1
11	154	100.0	7701	17	US-10-427-570A-9

C	12	154	100.0	7701	17	US-10-427-570A-9	Sequence 9, Appli
C	13	154	100.0	7701	18	US-10-734-947-1	Sequence 1, Appli
C	14	154	100.0	7701	18	US-10-734-947-1	Sequence 1, Appli
C	15	112	72.7	4974	9	US-09-906-209-17	Sequence 17, Appli
C	16	112	72.7	4974	9	US-09-906-209-17	Sequence 17, Appli
C	17	82.8	53.8	6611	10	US-09-934-900-26	Sequence 26, Appli
C	18	82.8	53.8	6611	10	US-09-934-900-26	Sequence 26, Appli
C	19	82.8	53.8	6611	19	US-10-981-293-26	Sequence 26, Appli
C	20	82.8	53.8	6611	19	US-10-981-293-26	Sequence 29, Appli
C	21	81	52.6	963	10	US-09-887-194A-29	Sequence 12, Appli
C	22	81	52.6	963	10	US-09-887-194A-29	Sequence 12, Appli
C	23	80	51.9	80	10	US-09-887-194A-12	Sequence 24, Appli
C	24	80	51.9	80	10	US-09-887-194A-12	Sequence 24, Appli
C	25	80	51.9	80	10	US-09-934-900-24	Sequence 24, Appli
C	26	80	51.9	80	10	US-09-934-900-24	Sequence 24, Appli
C	27	80	51.9	80	19	US-10-981-293-24	Sequence 24, Appli
C	28	80	51.9	80	19	US-10-981-293-24	Sequence 24, Appli
C	29	80	51.9	92	10	US-09-887-194A-14	Sequence 14, Appli
C	30	80	51.9	92	10	US-09-887-194A-14	Sequence 14, Appli
C	31	45.8	29.7	1717	10	US-09-887-194A-24	Sequence 24, Appli
C	32	45.8	29.7	1717	10	US-09-887-194A-24	Sequence 24, Appli
C	33	38.2	24.8	1251	17	US-10-389-647-277	Sequence 27, App
C	34	38.2	24.8	1251	17	US-10-389-647-277	Sequence 27, App
C	35	38	24.7	1581	15	US-10-156-761-6327	Sequence 6327, Ap
C	36	38	24.7	1581	15	US-10-156-761-6327	Sequence 6327, Ap
C	37	38	24.7	9025608	15	US-10-156-761-1	Sequence 1, Appli
C	38	38	24.7	9025608	15	US-10-156-761-1	Sequence 1, Appli
C	39	37	24.0	1821	18	US-10-437-963-43250	Sequence 43250, A
C	40	37	24.0	1821	18	US-10-437-963-43250	Sequence 43250, A
C	41	36.4	23.6	742	18	US-10-437-963-51952	Sequence 51952, A
C	42	36.4	23.6	742	18	US-10-437-963-51952	Sequence 51952, A
C	43	36	23.4	561	18	US-10-437-963-85043	Sequence 85043, A
C	44	36	23.4	561	18	US-10-437-963-85043	Sequence 85043, A
C	45	36	23.4	816	18	US-10-437-963-36912	Sequence 36912, A
C	46	36	23.4	816	18	US-10-437-963-36912	Sequence 36912, A
C	47	36	23.4	1153	18	US-10-425-115-141776	Sequence 141776,
C	48	36	23.4	1153	18	US-10-425-115-141776	Sequence 141776,
C	49	35.8	23.2	757	18	US-10-437-963-70150	Sequence 70150, A
C	50	35.8	23.2	757	18	US-10-437-963-70150	Sequence 70150, A
C	51	35.8	23.2	839	18	US-10-739-930-4978	Sequence 4978, Ap
C	52	35.8	23.2	839	18	US-10-739-930-4978	Sequence 4978, Ap
C	53	35.2	22.9	1308	15	US-10-156-761-7382	Sequence 7382, Ap
C	54	35.2	22.9	1308	15	US-10-156-761-7382	Sequence 7382, Ap
C	55	35.2	22.9	2730	17	US-10-260-238-1055	Sequence 1055, Ap
C	56	35.2	22.9	2730	17	US-10-260-238-1055	Sequence 1055, Ap
C	57	35	22.7	850	16	US-10-029-386-24874	Sequence 24874, A
C	58	35	22.7	850	16	US-10-029-386-24874	Sequence 24874, A
C	59	34.8	22.6	903	15	US-10-156-761-5558	Sequence 5558, Ap
C	60	34.8	22.6	903	15	US-10-156-761-5558	Sequence 5558, Ap
C	61	34.8	22.6	1681	16	US-10-271-889-7	Sequence 7, Appli
C	62	34.8	22.6	1681	16	US-10-271-889-7	Sequence 7, Appli
C	63	34.6	22.5	1217	18	US-10-437-963-96989	Sequence 96989, A
C	64	34.6	22.5	1217	18	US-10-437-963-96989	Sequence 96989, A
C	65	34.4	22.3	1699	18	US-10-437-963-52771	Sequence 52771, A
C	66	34.4	22.3	1699	18	US-10-437-963-52771	Sequence 52771, A
C	67	34.2	22.2	366	18	US-10-437-963-72120	Sequence 72120, A
C	68	34.2	22.2	366	18	US-10-437-963-72120	Sequence 72120, A
C	69	34.2	22.2	968	18	US-10-739-930-4744	Sequence 4744, Ap
C	70	34.2	22.2	968	18	US-10-739-930-4744	Sequence 4744, Ap
C	71	34.2	22.2	1245	17	US-10-260-238-3694	Sequence 3694, Ap
C	72	34.2	22.2	1245	17	US-10-260-238-3694	Sequence 3694, Ap
C	73	34	22.1	1775	18	US-10-437-963-51378	Sequence 51378, A
C	74	34	22.1	1775	18	US-10-437-963-51378	Sequence 51378, A
C	75	34	22.1	1786	18	US-10-437-963-68140	Sequence 68140, A
C	76	34	22.1	1786	18	US-10-437-963-68140	Sequence 68140, A
C	77	34	22.1	4758	18	US-10-437-963-97719	Sequence 97719, A
C	78	34	22.1	4758	18	US-10-437-963-97719	Sequence 97719, A
C	79	33.8	21.9	846	18	US-10-437-963-61	Sequence 61, Appli
C	80	33.8	21.9	846	18	US-10-437-963-61	Sequence 61, Appli
C	81	33.8	21.9	1386	17	US-10-104-047-1062	Sequence 1062, Ap
C	82	33.8	21.9	1386	17	US-10-104-047-1062	Sequence 1062, Ap
C	83	33.8	21.9	2100	18	US-10-437-963-330	Sequence 330, App
C	84	33.8	21.9	2100	18	US-10-437-963-330	Sequence 330, App

C 85	33.6	21.9	2821	9	US-09-812-350-40	Sequence 40, Appl
C 86	33.8	21.9	2821	9	US-09-812-350-40	Sequence 40, Appl
C 87	33.8	21.9	3107	9	US-09-812-350-39	Sequence 39, Appl
C 88	33.8	21.9	3107	9	US-09-812-350-39	Sequence 39, Appl
C 89	33.6	21.8	726	18	US-10-437-963-37821	Sequence 37821, A
C 90	33.6	21.8	726	18	US-10-437-963-37821	Sequence 37821, A
C 91	33.6	21.8	1233	17	US-10-282-122A-26073	Sequence 26073, A
C 92	33.6	21.8	1233	17	US-10-282-122A-26073	Sequence 26073, A
C 93	33.4	21.7	1105	17	US-10-282-122A-11328	Sequence 11328, A
C 94	33.4	21.7	1105	17	US-10-282-122A-11328	Sequence 11328, A
C 95	33.4	21.7	1227	18	US-10-437-963-60837	Sequence 60837, A
C 96	33.4	21.7	1227	18	US-10-437-963-60837	Sequence 60837, A
C 97	33.4	21.7	1574	17	US-10-115-831-157	Sequence 157, App
C 98	33.4	21.7	1574	17	US-10-115-831-157	Sequence 157, App
C 99	33.4	21.7	1726	18	US-10-437-963-100458	Sequence 100458, A
C 100	33.4	21.7	1726	18	US-10-437-963-100458	Sequence 100458, A

ALIGNMENTS

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RESULT 1
US-09-887-194A-13
; Sequence 13, Application US/09887194A
; Publication No. US20030036197A1
; GENERAL INFORMATION:
; APPLICANT: Glassman, Kimberly F.
; APPLICANT: Gordon-Kamm, William J.
; APPLICANT: Kinney, Anthony
; APPLICANT: Lowe, Keith S.
; APPLICANT: Nichols, Scott E.
; APPLICANT: Stecca, Kevin L.
; TITLE OF INVENTION: RECOMBINANT CONSTRUCTS AND THEIR USE IN REDUCING GENE EXPRESSION
; FILE REFERENCE: B01449 US NA
; CURRENT APPLICATION NUMBER: US/09/887,194A
; CURRENT FILING DATE: 2002-03-13
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 13
; LENGTH: 154
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: ELVISLIVES complementary
; US-09-887-194A-13

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	Query Match	100.0%;	Score 154;	DB 10;	Length 154;
	Best Local Similarity	100.0%;	Pred. No. 2.2e-37;		
	Matches 154;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1 CGGCCGGAGCTGTGCATCTCGCTCATCTGTCGAGTCCGCCGCCGAGCTGTGCATCTCGCT 				60
Db	1 CGGCCGGAGCTGTGCATCTCGCTCATCTGTCGAGTCCGCCGCCGAGCTGTGCATCTCGCT 				60
QY	61 CATCGTCAGTCCGCCGCCGCCGACTCGACGATGAGCGCAGATGACCAGCTCCGCCGCCG 				120
Db	61 CATCGTCAGTCCGCCGCCGCCGACTCGACGATGAGCGCAGATGACCAGCTCCGCCGCCG 				120
QY	121 ACTCGACGATGAGCGCAGATGACCAGCTCCGCCGCCG 				154
Db	121 ACTCGACGATGAGCGCAGATGACCAGCTCCGCCGCCG 				154

RESULT 2
US-09-887-194A-13/c
; Sequence 13, Application US/09887194A
; Publication No. US20030036197A1
; GENERAL INFORMATION:
; APPLICANT: Glassman, Kimberly F.
; APPLICANT: Gordon-Kamm, William J.
; APPLICANT: Kinney, Anthony
; APPLICANT: Lowe, Keith S.

```

; APPLICANT: Nichols, Scott E.
; APPLICANT: Stecca, Kevin L.
; TITLE OF INVENTION: RECOMBINANT CONSTRUCTS AND THEIR USE IN REDUCING GENE EXPRESSION
; FILE REFERENCE: BB1449 US NA
; CURRENT APPLICATION NUMBER: US/09/887,194A
; CURRENT FILING DATE: 2002-03-13
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 13
; LENGTH: 154
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: ELVISLIVES complementary
; OTHER INFORMATION: region of pKS133
US-09-887-194A-13

Query Match          100.0%; Score 154; DB 10; Length 154;
Best local Similarity 100.0%; Pred. No. 2.2e-37;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

[illegible]

```

RESULT 3
US-09-934-900-25
; Sequence 25, Application US/09934900
; Publication No. US20030054521A1
; GENERAL INFORMATION:
; APPLICANT: Booth, Russ
; APPLICANT: Cahoon, Rebecca E
; APPLICANT: Hiltz, William D
; APPLICANT: Kinney, Anthony
; APPLICANT: Yadav, Naren
; TITLE OF INVENTION: Nucleotide Sequences of a New Class of Diverged Delta-9 Stearoyl-
; TITLE OF INVENTION: ACP Desaturase
; FILE REFERENCE: B01476 US NA
; CURRENT APPLICATION NUMBER: US/09/934,900
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/226996
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 25
; LENGTH: 154
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: ELVISLIVES complementary
US-09-934-900-25

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Query Match	100.0%;	Score 154;	DB 10;	Length 154;
Best Local Similarity	100.0%;	Pred. No. 2.2e-37;		
Matches 154; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	CGGCCGAGCTGTCATCTCGCTCATCGTCGAGTCGGCGGCCGAGCTGTCATCTCGCT	60	
Db	1	CGGCCGAGCTGTCATCTCGCTCATCGTCGAGTCGGCGGCCGAGCTGTCATCTCGCT	60	
QY	61	CATCGTCGAGTCGGCGGCCGCGACTCGACCATGAGCGAGATGACCACTCCGGCCGCCG	120	
Db	61	CATCGTCGAGTCGGCGGCCGCGACTCGACCATGAGCGAGATGACCACTCCGGCCGCCG	120	

Qy 121 ACTGCAGATGAGCGAGATGACCAAGCTCCGGCGG 154
| | | | | | | | | | | | | | | | | | | | | |
Db 121 ACTGCAGATGAGCGAGATGACCAAGCTCCGGCGG 154

RESULT 4
US-09-934-900-25/c

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; Sequence 25, Application US/09934900
; Publication No. US20030054521A1
; GENERAL INFORMATION:

```

;
; APPLICANT: Booth, Russ
; APPLICANT: Cahoon, Rebecca E
; APPLICANT: Hiltz, William D
; APPLICANT: Kinney, Anthony

;; TITLE OF INVENTION: Nucleotide Sequences of a New Class of Diverged Delta-9 Stearoyl-
;; TITLE OF INVENTION: ACP Desaturase

;; CURRENT APPLICATION NUMBER: US/09/934,900
; CURRENT FILING DATE: 2001-08-22

PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 26

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; SEQ ID NO 25
; LENGTH: 154

```

```

; NAME: DATA
; ORGANISM: Artificial Sequence
; FEATURE:

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1  OTHER INFORMATION:  region of PKS133
2  US-09-934-900-25
3  OTHER INFORMATION:  region of PKS133
4  US-09-934-900-25
5  OTHER INFORMATION:  region of PKS133
6  US-09-934-900-25
7  OTHER INFORMATION:  region of PKS133
8  US-09-934-900-25
9  OTHER INFORMATION:  region of PKS133
10 US-09-934-900-25
11 OTHER INFORMATION:  region of PKS133
12 US-09-934-900-25
13 OTHER INFORMATION:  region of PKS133
14 US-09-934-900-25
15 OTHER INFORMATION:  region of PKS133
16 US-09-934-900-25
17 OTHER INFORMATION:  region of PKS133
18 US-09-934-900-25
19 OTHER INFORMATION:  region of PKS133
20 US-09-934-900-25
21 OTHER INFORMATION:  region of PKS133
22 US-09-934-900-25
23 OTHER INFORMATION:  region of PKS133
24 US-09-934-900-25
25 OTHER INFORMATION:  region of PKS133
26 US-09-934-900-25
27 OTHER INFORMATION:  region of PKS133
28 US-09-934-900-25
29 OTHER INFORMATION:  region of PKS133
30 US-09-934-900-25
31 OTHER INFORMATION:  region of PKS133
32 US-09-934-900-25
33 OTHER INFORMATION:  region of PKS133
34 US-09-934-900-25
35 OTHER INFORMATION:  region of PKS133
36 US-09-934-900-25
37 OTHER INFORMATION:  region of PKS133
38 US-09-934-900-25
39 OTHER INFORMATION:  region of PKS133
40 US-09-934-900-25
41 OTHER INFORMATION:  region of PKS133
42 US-09-934-900-25
43 OTHER INFORMATION:  region of PKS133
44 US-09-934-900-25
45 OTHER INFORMATION:  region of PKS133
46 US-09-934-900-25
47 OTHER INFORMATION:  region of PKS133
48 US-09-934-900-25
49 OTHER INFORMATION:  region of PKS133
50 US-09-934-900-25
51 OTHER INFORMATION:  region of PKS133
52 US-09-934-900-25
53 OTHER INFORMATION:  region of PKS133
54 US-09-934-900-25
55 OTHER INFORMATION:  region of PKS133
56 US-09-934-900-25
57 OTHER INFORMATION:  region of PKS133
58 US-09-934-900-25
59 OTHER INFORMATION:  region of PKS133
60 US-09-934-900-25
61 OTHER INFORMATION:  region of PKS133
62 US-09-934-900-25
63 OTHER INFORMATION:  region of PKS133
64 US-09-934-900-25
65 OTHER INFORMATION:  region of PKS133
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67 OTHER INFORMATION:  region of PKS133
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69 OTHER INFORMATION:  region of PKS133
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71 OTHER INFORMATION:  region of PKS133
72 US-09-934-900-25
73 OTHER INFORMATION:  region of PKS133
74 US-09-934-900-25
75 OTHER INFORMATION:  region of PKS133
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77 OTHER INFORMATION:  region of PKS133
78 US-09-934-900-25
79 OTHER INFORMATION:  region of PKS133
80 US-09-934-900-25
81 OTHER INFORMATION:  region of PKS133
82 US-09-934-900-25
83 OTHER INFORMATION:  region of PKS133
84 US-09-934-900-25
85 OTHER INFORMATION:  region of PKS133
86 US-09-934-900-25
87 OTHER INFORMATION:  region of PKS133
88 US-09-934-900-25
89 OTHER INFORMATION:  region of PKS133
90 US-09-934-900-25
91 OTHER INFORMATION:  region of PKS133
92 US-09-934-900-25
93 OTHER INFORMATION:  region of PKS133
94 US-09-934-900-25
95 OTHER INFORMATION:  region of PKS133
96 US-09-934-900-25
97 OTHER INFORMATION:  region of PKS133
98 US-09-934-900-25
99 OTHER INFORMATION:  region of PKS133
100 US-09-934-900-25

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Query Match	100.0%;	Score 154;	DB 10;	Length 154;
Best Local Similarity	100.0%;	Pred. No. 2.2e-37;		
Matches 154;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY 1 CGGCCGGAGCTGGTCATCTCGCTCATCGTGCAGTCCGCGCGGAGCTGGTCATCTCGCT 60
| | | | |
DB 154 CGGCCGGAGCTGGTCATCTCGCTCATCGTGCAGTCCGCGCGGAGCTGGTCATCTCGCT 95

```

QY      61 CATCGTCAGTCCGCGCGCCCGCGCGCTCGACGATGAGCGAGATGACCACTCCGGCGCGCC 120
      |||||
Db      94 CATCGTCAGTCCGCGCGCCCGCGCGCTCGACGATGAGCGAGATGACCACTCCGGCGCGCC 35

```

QY 121 ACTTCGACGATGAGCGAGATGACCAGCTCCGCCG 154
| | | | | | | | | | | | | | | | | | | |
Db 34 ACTTCGACGATGAGCGAGATGACCAGCTCCGCCG 1

RESULT 5
US-10-734-947-7

Publication No. US20040128714A1
GENERAL INFORMATION:
ADDITONAL INFORMATION: *Enfer*

APPLICANT: McConigle, Brian
TITLE OF INVENTION: METHOD OF DECREASING LIQUIRITIGENIN-DERIVED ISOFLAVONES RELATIVE TO TOTAL ISOFLAVONES IN PLANTS PRODUCING REDUCED RATIO OF LIQUIRITIGENIN-DERIVED ISOFLAVONES RELATIVE TO TOTAL ISOFLAVONES
TITLE OF INVENTION: LIQUIRITIGENIN-DERIVED ISOFLAVONES RELATIVE TO TOTAL ISOFLAVONES
FILING DATE: 08/15/2013

; CURRENT FILING DATE: 2003-12-11
 ; PRIOR APPLICATION NUMBER: US 60/433,433
 ; PRIOR FILING DATE: 2003-12-12

```

; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 7

```

LENGTH: 154
TYPE: DNA
ORGANISM: R

```

; FEATURE: Artificial sequence containing a NotI site flanked by two
; OTHER INFORMATION:

```

OTHER INFORMATION: 36-nucleotide repeats and having an EagI site at each end.
US-10-734-947-7

Query Match	100.0%;	Score 154;	DB 18;	Length 154;
Best Local Similarity	100.0%;	Pred. No. 2.2e-37;		
Matches 154; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

QY 1 CGGCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCCGGAGCTGGTCATCTCGCT 600

Db 1 CGGCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCCGGAGCTGGTCATCTCGCT 600

```

      61 CATCGTCGAGTCGGCGCGCCGCACTCGACGATGAGCGAGTACCAGCTCCGGCCCG 120
      |||
      61 CATCGTCGAGTCGGCGCGCCGCACTCGACGATGAGCGAGTACCAGCTCCGGCCCG 120
      |||

```

```

QY      121  ACTCGACGATGAGCGAGATGACCGAGCTCCGGCCG  154
          |||||
Db      121  ACTCGACGATGAGCGAGATGACCGAGCTCCGGCCG  154

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US-10-734-947-7/c

Sequence 7, Application US/1073494A7
Publication No. US20040128741A1
GENERAL INFORMATION:
APPLICANT: McConigle, Brian
FIELD OF INVENTION: METHOD OF PRODUCING

TITLE OF INVENTION: METHOD OF DECREASING LIQUIRITIGENIN-DERIVED ISOFLAVONES RELATIVE
TITLE OF INVENTION: TOTAL ISOFLAVONES IN PLANTS AND PLANTS PRODUCING REDUCED RATIO O
TITLE OF INVENTION: LIQUIRITIGENIN-DERIVED ISOFLAVONES RELATIVE TO TOTAL ISOFLAVONES
FILE REFERENCE: BB1535 US NA
CURRENT APPLICATION NUMBER: US/10/7734 947

CURRENT APPLICATION NUMBER: US/10/734,947
CURRENT FILING DATE: 2003-12-11
PRIOR APPLICATION NUMBER: US 60/433,433
PRIOR FILING DATE: 2002-12-13
NUMBER OF SEQ ID NOS: 8

```
SOFTWARE: Microsoft Office 97
SEQ ID NO 7
LENGTH: 154
```

TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:

OTHER INFORMATION: Artificial sequence containing a NotI site flanked by two
OTHER INFORMATION: 36-nucleotide repeats and having an EagI site at each end.
US-10-734-947-7

Query Match	100.0%;	Score 154;	DB 18;	Length 154;
Best Local Similarity	100.0%;	Pred. No. 2.2e-37;		
Matches 154; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

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QY      1 CGGCCGAGCTGTCATCTCGCTCATCGTCGAGTCGGCCGGAGCTGTCATCTCGCT 60
        |||||
Db      154 CGGCCGAGCTGTCATCTCGCTCATCGTCGAGTCGGCCGGAGCTGTCATCTCGCT 95

```

Dy 61 CATGTCGAGTCCGGCGGCCGCCTGACCATGATGACCAAGCTCCGGCGCCG 120
|||
Db 94 CATGTCGAGTCCGGCGGCCGCCTGACCATGATGACCAAGCTCCGGCGCCG 35

QY	121	ACTCGACGATGAGCGAGATGACCAAGCTCCGCGCG	154
Db	34	ACTCGACGATGAGCGAGATGACCAAGCTCCGCGCG	1

US-10-981-293-25
; Sequence 25, A

Publication No. US20050066390A1
GENERAL INFORMATION:
APPLICANT: Booth, Russ
APPLICANT: Cahoon, Rebecca E

APPLICANT: Yadav, Naren
TITLE OF INVENTION: Nucleotide Sequences of a New Class of Diverged Delta-9 Stearoyl-

```

; TITLE OF INVENTION: ACP Desaturase
; FILE REFERENCE: BB1476 US NA
; CURRENT APPLICATION NUMBER: US/10/981,293
; PRIOR FILING DATE: 2004-11-04
; PRIOR APPLICATION NUMBER: US/09/934,900
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/226996
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 25
; LENGTH: 154
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: ELVISLIVES complementary
; OTHER INFORMATION: region of pKS133
US-10-981-293-25
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```
Query Match
Best Local Similarity 100.0%; Score 154; DB 19; Length 154;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 CGGCCGAGCTGTGTCATCTCGCTCATCGTCGAGTCGGCGCCGAGCTGTGTCATCTCGCT 60
    |||
Db 1 CGGCCGAGCTGTGTCATCTCGCTCATCGTCGAGTCGGCGCCGAGCTGTGTCATCTCGCT 60

QY 61 CATCGTCGAGTCGGCGCCGCGCCGACTCGACGATGAGCGAGATGACCACTCCGGCCGCG 120
    |||
Db 61 CATCGTCGAGTCGGCGCCGCGCCGACTCGACGATGAGCGAGATGACCACTCCGGCCGCG 120

QY 121 ACTCGACGATGAGCGAGATGACCACTCCGGCCG 154
    |||
Db 121 ACTCGACGATGAGCGAGATGACCACTCCGGCCG 154
```

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RESULT 8
US-10-981-293-25/c
; Sequence 25, Application US/10981293
; Publication No. US20050066390A1
; GENERAL INFORMATION:
; APPLICANT: Booth, Russ
; APPLICANT: Cahoon, Rebecca E
; APPLICANT: Hitz, William D
; APPLICANT: Kinney, Anthony
; APPLICANT: Yadav, Naren
; TITLE OF INVENTION: Nucleotide Sequences of a New Class of Diverged Delta-9 Stearoyl-
; TITLE OF INVENTION: ACP Desaturase
; FILE REFERENCE: BB1476 US NA
; CURRENT APPLICATION NUMBER: US/10/981,293
; PRIOR FILING DATE: 2004-11-04
; PRIOR APPLICATION NUMBER: US/09/934,900
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/226996
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 25
; LENGTH: 154
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: ELVISLIVES complementary
; OTHER INFORMATION: region of pKS133
US-10-981-293-25
```

```
Query Match
Best Local Similarity 100.0%; Score 154; DB 19; Length 154;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGGCCGAGCTGTGTCATCTCGCTCATCGTCGAGTCGGCGCCGAGCTGTGTCATCTCGCT 60
    |||
Db 154 CGGCCGAGCTGTGTCATCTCGCTCATCGTCGAGTCGGCGCCGAGCTGTGTCATCTCGCT 95
```

```
QY 61 CATCGTCGAGTCGGCGCCGCGCCGACTCGACGATGAGCGAGATGACCACTCCGGCCGCG 120
    |||
Db 94 CATCGTCGAGTCGGCGCCGCGCCGACTCGACGATGAGCGAGATGACCACTCCGGCCGCG 35

QY 121 ACTCGACGATGAGCGAGATGACCACTCCGGCCG 154
    |||
Db 34 ACTCGACGATGAGCGAGATGACCACTCCGGCCG 1
```

```
RESULT 9
US-10-459-159-1
; Sequence 1, Application US/10459159
; Publication No. US20040006795A1
; GENERAL INFORMATION:
; APPLICANT: Mcgonigle, Brian
; APPLICANT: Odell, Joan T.
; TITLE OF INVENTION: METHOD TO INCREASE THE ISOFLAVONOID LEVELS IN PLANTS AND PLANTS
; TITLE OF INVENTION: PRODUCING INCREASED LEVELS OF ISOFLAVONIDS
; FILE REFERENCE: BB1526 US NA
; CURRENT APPLICATION NUMBER: US/10/459,159
; PRIOR FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: 60/388,280
; PRIOR FILING DATE: 2002-06-13
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 1
; LENGTH: 7701
; TYPE: DNA
; ORGANISM: expression vector pKS151
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (6516)..(6516)
; OTHER INFORMATION: n = A, C, G, or T
US-10-459-159-1
```

```
Query Match
Best Local Similarity 100.0%; Score 154; DB 17; Length 7701;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 CGGCCGAGCTGTGTCATCTCGCTCATCGTCGAGTCGGCGCCGAGCTGTGTCATCTCGCT 60
    |||
Db 5451 CGGCCGAGCTGTGTCATCTCGCTCATCGTCGAGTCGGCGCCGAGCTGTGTCATCTCGCT 5510

QY 61 CATCGTCGAGTCGGCGCCGCGCCGACTCGACGATGAGCGAGATGACCACTCCGGCCGCG 120
    |||
Db 5511 CATCGTCGAGTCGGCGCCGCGCCGACTCGACGATGAGCGAGATGACCACTCCGGCCGCG 5570

QY 121 ACTCGACGATGAGCGAGATGACCACTCCGGCCG 154
    |||
Db 5571 ACTCGACGATGAGCGAGATGACCACTCCGGCCG 5604
```

```
RESULT 10
US-10-459-159-1/c
; Sequence 1, Application US/10459159
; Publication No. US20040006795A1
; GENERAL INFORMATION:
; APPLICANT: Mcgonigle, Brian
; APPLICANT: Odell, Joan T.
; TITLE OF INVENTION: METHOD TO INCREASE THE ISOFLAVONOID LEVELS IN PLANTS AND PLANTS
; TITLE OF INVENTION: PRODUCING INCREASED LEVELS OF ISOFLAVONIDS
; FILE REFERENCE: BB1526 US NA
; CURRENT APPLICATION NUMBER: US/10/459,159
; PRIOR FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: 60/388,280
; PRIOR FILING DATE: 2002-06-13
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 1
; LENGTH: 7701
; TYPE: DNA
; ORGANISM: expression vector pKS151
```

```
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (6516) ..(6516)
; OTHER INFORMATION: n = A, C, G, or T
US-10-459-159-1
```

```
Query Match      100.0%; Score 154; DB 17; Length 7701;
Best Local Similarity 100.0%; Pred. No. 1.8e-37;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 CGCCCGAGCTGCTCATCTCGCTCATCTCGAGTCGGCGCCGAGCTGTCTCATCTCGCT 60
DB 5604 CGCCCGAGCTGCTCATCTCGCTCATCTCGAGTCGGCGCCGAGCTGTCTCATCTCGCT 5545
OY 61 CATCTCGAGTCGGCGCCGCGCCGACTCGAGTCGATGACGAGATGACCACTCCGCGCCG 120
DB 5544 CATCTCGAGTCGGCGCCGCGCCGACTCGAGTCGATGACGAGATGACCACTCCGCGCCG 5485
OY 121 ACTCGACGATGACGAGATGACCACTCCGCGCCG 154
DB 5484 ACTCGACGATGACGAGATGACCACTCCGCGCCG 5451
```

RESULT 11
US-10-427-570A-9

```
; Sequence 9, Application US/10427570A
; Publication No. US20040010818A1
```

```
; GENERAL INFORMATION:
; APPLICANT: McGonigle, Brian
; APPLICANT: Maxwell, Carl A.
; APPLICANT: Hession, Aileen O.
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH A SUPPRESSED TRITERPENE LEVEL
; FILE REFERENCE: BB1523 US NA
; CURRENT FILING DATE: 2003-05-01
; PRIOR APPLICATION NUMBER: US/10/427,570A
; PRIOR FILING DATE: 2002-05-09
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 9
; LENGTH: 7701
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: expression vector pKS151
; FEATURE:
; NAME/KEY: Unsure
; LOCATION: (6516)
; OTHER INFORMATION: n = A, C, G, or T
US-10-427-570A-9
```

```
Query Match      100.0%; Score 154; DB 17; Length 7701;
Best Local Similarity 100.0%; Pred. No. 1.8e-37;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 CGCCCGAGCTGCTCATCTCGCTCATCTCGAGTCGGCGCCGAGCTGTCTCATCTCGCT 60
DB 5451 CGCCCGAGCTGCTCATCTCGCTCATCTCGAGTCGGCGCCGAGCTGTCTCATCTCGCT 5510
OY 61 CATCTCGAGTCGGCGCCGCGCCGACTCGAGTCGATGACGAGATGACCACTCCGCGCCG 120
DB 5511 CATCTCGAGTCGGCGCCGCGCCGACTCGAGTCGATGACGAGATGACCACTCCGCGCCG 5570
OY 121 ACTCGACGATGACGAGATGACCACTCCGCGCCG 154
DB 5571 ACTCGACGATGACGAGATGACCACTCCGCGCCG 5604
```

RESULT 12
US-10-427-570A-9/c
; Sequence 9, Application US/10427570A
; Publication No. US20040010818A1
; GENERAL INFORMATION:

```
; APPLICANT: McGonigle, Brian
; APPLICANT: Maxwell, Carl A.
; APPLICANT: Hession, Aileen O.
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH A SUPPRESSED TRITERPENE LEVEL
; FILE REFERENCE: BB1523 US NA
; CURRENT FILING DATE: US/10/427,570A
; PRIOR APPLICATION NUMBER: 60/379,361
; PRIOR FILING DATE: 2002-05-09
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 9
; LENGTH: 7701
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: expression vector pKS151
; FEATURE:
; NAME/KEY: Unsure
; LOCATION: (6516)
; OTHER INFORMATION: n = A, C, G, or T
US-10-427-570A-9
```

```
Query Match      100.0%; Score 154; DB 17; Length 7701;
Best Local Similarity 100.0%; Pred. No. 1.8e-37;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 CGCCCGAGCTGCTCATCTCGCTCATCTCGAGTCGGCGCCGAGCTGTCTCATCTCGCT 60
DB 5604 CGCCCGAGCTGCTCATCTCGCTCATCTCGAGTCGGCGCCGAGCTGTCTCATCTCGCT 5545
OY 61 CATCTCGAGTCGGCGCCGCGCCGACTCGAGTCGATGACGAGATGACCACTCCGCGCCG 120
DB 5544 CATCTCGAGTCGGCGCCGCGCCGACTCGAGTCGATGACGAGATGACCACTCCGCGCCG 5485
OY 121 ACTCGACGATGACGAGATGACCACTCCGCGCCG 154
DB 5484 ACTCGACGATGACGAGATGACCACTCCGCGCCG 5451
```

RESULT 13

US-10-734-947-1

```
; Sequence 1, Application US/10734947
; Publication No. US20040128714A1
```

```
; GENERAL INFORMATION:
; APPLICANT: McGonigle, Brian
; TITLE OF INVENTION: METHOD OF DECREASING LIQUIRITIGENIN-DERIVED ISOFLAVONES RELATIVE
; TITLE OF INVENTION: TOTAL ISOFLAVONES IN PLANTS AND PLANTS PRODUCING REDUCED RATIO O
; TITLE OF INVENTION: LIQUIRITIGENIN-DERIVED ISOFLAVONES RELATIVE TO TOTAL ISOFLAVONES
; FILE REFERENCE: BB1535 US NA
; CURRENT FILING DATE: US/10/734,947
; PRIOR FILING DATE: 2003-12-11
; PRIOR APPLICATION NUMBER: US 60/433,433
; PRIOR FILING DATE: 2002-12-13
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 1
; LENGTH: 7701
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Expression Vector pKS151
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (6516) ..(6516)
; OTHER INFORMATION: n = A, C, G, or T
US-10-734-947-1
```

```
Query Match      100.0%; Score 154; DB 18; Length 7701;
Best Local Similarity 100.0%; Pred. No. 1.8e-37;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

OY 1 CGCCCGAGCTGCTCATCTCGCTCATCTCGAGTCGGCGCCGAGCTGTCTCATCTCGCT 60

```
Db 5451 CCGCCGAGCTGGTCACTCTCGCTCATCGTCGAGTCGGCGCCGAGAGCTGGTCACTCTCGCT 5510
QY 61 CATCGTCGAGTCGGCGCCCGCCGCACTCGACGATGAGCGAGATGACCAGCTCCGCGCCG 120
Db 5511 CATCGTCGAGTCGGCGCCCGCCGCACTCGACGATGAGCGAGATGACCAGCTCCGCGCCG 5570
QY 121 ACTCGACGATGAGCGAGATGACCACTCCGCGCCG 154
Db 5571 ACTCGACGATGAGCGAGATGACCACTCCGCGCCG 5604
```

RESULT 14
US-10-734-947-1/c

```
; Sequence 1, Application US/10734947
; Publication No. US20040128714A1
; GENERAL INFORMATION:
; APPLICANT: McGonigle, Brian
; TITLE OF INVENTION: METHOD OF DECREASING LIQUIRITIGENIN-DERIVED ISOFLAVONES RELATIVE
; TITLE OF INVENTION: TOTAL ISOFLAVONES IN PLANTS AND PLANTS PRODUCING REDUCED RATIO O
; TITLE OF INVENTION: LIQUIRITIGENIN-DERIVED ISOFLAVONES RELATIVE TO TOTAL ISOFLAVONES
; FILE REFERENCE: BB1535 US NA
; CURRENT APPLICATION NUMBER: US/10/734,947
; PRIOR FILING DATE: 2003-12-11
; PRIOR APPLICATION NUMBER: US 60/433,433
; PRIOR FILING DATE: 2002-12-13
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 1
; LENGTH: 7701
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Expression Vector pKS151
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (6516)..(6516)
; OTHER INFORMATION: n = A, C, G, or T
US-10-734-947-1
```

Query Match 100.0%; Score 154; DB 18; Length 7701;
Best Local Similarity 100.0%; Pred. No. 1.8e-37;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 CCGCCGAGCTGGTCACTCTCGCTCATCGTCGAGTCGGCGCCGAGAGCTGGTCACTCTCGCT 60
Db 5604 CCGCCGAGCTGGTCACTCTCGCTCATCGTCGAGTCGGCGCCGAGAGCTGGTCACTCTCGCT 5545
QY 61 CATCGTCGAGTCGGCGCCCGCCGCACTCGACGATGAGCGAGATGACCAGCTCCGCGCCG 120
Db 5544 CATCGTCGAGTCGGCGCCCGCCGCACTCGACGATGAGCGAGATGACCAGCTCCGCGCCG 5485
QY 121 ACTCGACGATGAGCGAGATGACCACTCCGCGCCG 154
Db 5484 ACTCGACGATGAGCGAGATGACCACTCCGCGCCG 5451
```

RESULT 15

```
US-09-906-209-17
; Sequence 17, Application US/09906209
; Patent No. US20020165385A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Butler, Steve
; APPLICANT: Carlson, Tom
; APPLICANT: Ilag, Lawrence L.
; TITLE OF INVENTION: Plastidic Phosphoglucumutase Genes
; FILE REFERENCE: BB1451 NA
; CURRENT APPLICATION NUMBER: US/09/906,209
; PRIOR FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 60/218,712
; PRIOR FILING DATE: JULY 17, 2000
; NUMBER OF SEQ ID NOS: 17
```

```
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 17
; LENGTH: 4974
; TYPE: DNA
; ORGANISM: synthetic construct
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (3951)
; OTHER INFORMATION: n = A, C, G, or T
US-09-906-209-17
```

Query Match 72.7%; Score 112; DB 9; Length 4974;
Best Local Similarity 100.0%; Pred. No. 9.8e-25;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 CCGCCGAGCTGGTCACTCTCGCTCATCGTCGAGTCGGCGCCGAGAGCTGGTCACTCTCGCT 60
Db 4863 CCGCCGAGCTGGTCACTCTCGCTCATCGTCGAGTCGGCGCCGAGAGCTGGTCACTCTCGCT 4922
QY 61 CATCGTCGAGTCGGCGCCCGCCGCACTCGACGATGAGCGAGATGACCAGCTCC 112
Db 4923 CATCGTCGAGTCGGCGCCCGCCGCACTCGACGATGAGCGAGATGACCAGCTCC 4974
```

RESULT 16
US-09-906-209-17/c

```
; Sequence 17, Application US/09906209
; Patent No. US20020165385A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Butler, Steve
; APPLICANT: Carlson, Tom
; APPLICANT: Ilag, Lawrence L.
; TITLE OF INVENTION: Plastidic Phosphoglucumutase Genes
; FILE REFERENCE: BB1451 NA
; CURRENT APPLICATION NUMBER: US/09/906,209
; PRIOR FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 60/218,712
; PRIOR FILING DATE: JULY 17, 2000
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 17
; LENGTH: 4974
; TYPE: DNA
; ORGANISM: synthetic construct
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (3951)
; OTHER INFORMATION: n = A, C, G, or T
US-09-906-209-17
```

Query Match 72.7%; Score 112; DB 9; Length 4974;
Best Local Similarity 100.0%; Pred. No. 9.8e-25;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 43 GGAGCTGGTCACTCTCGCTCATCGTCGAGTCGGCGCCCGCACTCGACGATGAGCGAGAT 102
Db 4974 GGAGCTGGTCACTCTCGCTCATCGTCGAGTCGGCGCCCGCACTCGACGATGAGCGAGAT 4915
QY 103 GACCACTCCGCGCCCGCCGCACTCGACGATGAGCGAGATGACCAGCTCCGCGCCG 154
Db 4914 GACCACTCCGCGCCCGCCGCACTCGACGATGAGCGAGATGACCAGCTCCGCGCCG 4863
```

RESULT 17

```
US-09-934-900-26
; Sequence 26, Application US/09934900
; Publication No. US20030054521A1
; GENERAL INFORMATION:
; APPLICANT: Booth, Russ
; APPLICANT: Cahoon, Rebecca E
; APPLICANT: Hitz, William D
; APPLICANT: Kinney, Anthony
```

```

; APPLICANT: Yadav, Naren
; TITLE OF INVENTION: Nucleotide Sequences of a New Class of Diverged Delta-9 Stearoyl
; TITLE OF INVENTION: ACP Desaturase
; FILE REFERENCE: BB1476 US NA
; CURRENT APPLICATION NUMBER: US/09/934,900
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/226996
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 26
; LENGTH: 6611
; TYPE: DNA
; ORGANISM: Plasmid pBS68
; FEATURE:
; NAME/KEY: Unsure
; LOCATION: (4436)..(4436)
; OTHER INFORMATION: n = A, C, G, or T
US-09-934-900-26

```

Query Match	53.8%	Score 82.8;	DB 10;	Length 6611;
Best Local Similarity	97.7%;	Pred. No. 7e-16;		
Matches 84; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;

Oy 1 CGGCGGAGCTGGTCAATTCGGCTCATCGTCGAGTCGGCGGCGGAGCTGGTCAATTCGCT 60

Db 5348 CGGCGGAGCTGGTCAATTCGGCTCATCGTCGAGTCGGCGGCGGAGCTGGTCAATTCGCT 5407

Qy	61	CATCGTCAGTCGGCGCCGCGCACT	86
Db	5408	CATCGTCAGTCGGCGCCGCTGACT	5433

```

RESULT 18
US-09-934-900-26/c
; Sequence 26, Application US/09934900
; Publication No. US20030054521A1
; GENERAL INFORMATION:
; APPLICANT: Booth, Russ
; APPLICANT: Cahoon, Rebecca E
; APPLICANT: Hitz, William D
; APPLICANT: Kinney, Anthony
; APPLICANT: Yadav, Naren
; TITLE OF INVENTION: Nucleotide Sequences of a New Class of Diverged Delta-9 Stearoyl
; TITLE OF INVENTION: ACP Desaturase
; FILE REFERENCE: BB1476 US NA
; CURRENT APPLICATION NUMBER: US/09/934,900
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/226996
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 26
; LENGTH: 6611
; TYPE: DNA
; ORGANISM: Plasmid pBS68
; FEATURE:
; NAME/KEY: Unsure
; LOCATION: (4436)..(4436)
; OTHER INFORMATION: n = A, C, G, or T
US-09-934-900-26

```

Query Match	53.8%	Score 82.8;	DB 10;	Length 6611;
Best Local Similarity	97.7%;	Pred. No. 7e-16;		
Matches 84; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;

Oy	69	A	G	T	C	G	C	G	C	C	G	A	C	T	G	A	T	G	A	G	C	G	A	T	G	A	C	C	T	C	G	G	C	C	G	A	C	T	G	A	C	G		128			
Db	5433	A	C	T	C	A	G	C	G	C	C	G	A	C	T	G	A	T	G	A	G	C	G	A	T	G	A	C	C	A	C	T	C	G	G	C	C	G	A	C	T	G	A	C	G		5374

QY	129	ATGAGCGAGATGACCACTCCGCCG	154
Db	5373	ATGAGCGAGATGACCACTCCGCCG	5348

```

RESULT 19
US-10-981-293-26
; Sequence 26, Application US/10981293
; Publication No. US20050066390A1
; GENERAL INFORMATION:
; APPLICANT: Booth, Russ
; APPLICANT: Cahoon, Rebecca B
; APPLICANT: Hitz, William D
; APPLICANT: Kinney, Anthony
; APPLICANT: Yadav, Naren
; TITLE OF INVENTION: Nucleotide Sequences of a New Class of Diverged Delta-9 Stearoyl-
; TITLE OF INVENTION: ACP Desaturase
; FILE REFERENCE: BB1476 US NA
; CURRENT APPLICATION NUMBER: US/10/981,293
; CURRENT FILING DATE: 2004-11-04
; PRIOR APPLICATION NUMBER: US/09/934,900
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/226996
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 26
; LENGTH: 6611
; TYPE: DNA
; ORGANISM: Plasmid pBS68
; FEATURE:
; NAME/KEY: Unsure
; LOCATION: (4436)..(4436)
; OTHER INFORMATION: n = A, C, G, or T
US-10-981-293-26

```

Query Match	53.8%;	Score 82.8;	DB 19;	Length 6611;
Best Local Similarity	97.7%;	Pred. No. 7e-16;		
Matches 84;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;

OY

1 CGCCGAGCTGGTCATCTCGCTCATCTGCAGTGGCGGCCGAGCTGTTCATCTCGCT
|||||
5348 CGCCGAGCTGGTCATCTCGCTCATCTGCAGTGGCGGCCGAGCTGTTCATCTCGCT 5407

D6

QY 61 CATGTCAGTCGGCGCCGCGACT 86
|||
Db 5408 CATGTCAGTCGGCGCCGCGTACT 5433

```

RESULT 20
US-10-981-293-26/c
; Sequence 26, Application US/10981293
; Publication No. US20050066390A1
; GENERAL INFORMATION:
; APPLICANT: Booth, Russ
; APPLICANT: Cahoon, Rebecca E
; APPLICANT: Hitz, William D
; APPLICANT: Kinney, Anthony
; APPLICANT: Yadav, Naren
; TITLE OF INVENTION: Nucleotide Sequences of a New Class of Diverged Delta-9 Stearoyl-
; FILE REFERENCE: BBI476 US NA
; CURRENT APPLICATION NUMBER: US/10/981,293
; CURRENT FILING DATE: 2004-11-04
; PRIOR APPLICATION NUMBER: US/09/934,900
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/226996
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 26
; LENGTH: 6611
; TYPE: DNA
; ORGANISM: Plasmid pBS68
; FEATURE:
; NAME/KEY: Unsure
;

```



```
; FILE REFERENCE: BBI449 US NA
; CURRENT APPLICATION NUMBER: US/09/887,194A
; CURRENT FILING DATE: 2002-03-13
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 12
; LENGTH: 80
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: ELVISLIVES complementary
US-09-887-194A-12

Query Match          51.9%; Score 80; DB 10; Length 80;
Best Local Similarity 100.0%; Pred. No. 6.3e-15;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 CGCCGAGCTGTCATCTCGCTCATCTGTCGAGTCGCGCGCCGCCGACTCGACGATGAGC 97
    |||
DB 80 CGCCGAGCTGTCATCTCGCTCATCTGTCGAGTCGCGCGCCGCCGACTCGACGATGAGC 21

QY 98 GAGATGACCACTCCGCGCC 117
    |||
DB 20 GAGATGACCACTCCGCGCC 1

RESULT 25
US-09-934-900-24
; Sequence 24, Application US/09934900
; Publication No. US20030054521A1
; GENERAL INFORMATION:
; APPLICANT: Booth, Russ
; APPLICANT: Cahoon, Rebecca E
; APPLICANT: Hitz, William D
; APPLICANT: Kinney, Anthony
; APPLICANT: Yadav, Naren
; TITLE OF INVENTION: Nucleotide Sequences of a New Class of Diverged Delta-9 Stearoyl-
; TITLE OF INVENTION: ACP Desaturase
; FILE REFERENCE: BBI476 US NA
; CURRENT APPLICATION NUMBER: US/09/934,900
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/226996
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 24
; LENGTH: 80
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: ELVISLIVES complementary
US-09-934-900-24

Query Match          51.9%; Score 80; DB 10; Length 80;
Best Local Similarity 100.0%; Pred. No. 6.3e-15;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 CGCCGAGCTGTCATCTCGCTCATCTGTCGAGTCGCGCGCCGCCGACTCGACGATGAGC 97
    |||
DB 1 CGCCGAGCTGTCATCTCGCTCATCTGTCGAGTCGCGCGCCGCCGACTCGACGATGAGC 60

QY 98 GAGATGACCACTCCGCGCC 117
    |||
DB 61 GAGATGACCACTCCGCGCC 80

RESULT 26
US-09-934-900-24/c
; Sequence 24, Application US/09934900
; Publication No. US20030054521A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Booth, Russ
; APPLICANT: Cahoon, Rebecca E
; APPLICANT: Hitz, William D
; APPLICANT: Kinney, Anthony
; APPLICANT: Yadav, Naren
; TITLE OF INVENTION: Nucleotide Sequences of a New Class of Diverged Delta-9 Stearoyl-
; TITLE OF INVENTION: ACP Desaturase
; FILE REFERENCE: BBI476 US NA
; CURRENT APPLICATION NUMBER: US/09/934,900
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/226996
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 24
; LENGTH: 80
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: ELVISLIVES complementary
US-10-981-293-24

Query Match          51.9%; Score 80; DB 19; Length 80;
Best Local Similarity 100.0%; Pred. No. 6.3e-15;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 CGCCGAGCTGTCATCTCGCTCATCTGTCGAGTCGCGCGCCGCCGACTCGACGATGAGC 97
    |||
DB 1 CGCCGAGCTGTCATCTCGCTCATCTGTCGAGTCGCGCGCCGCCGACTCGACGATGAGC 60

RESULT 27
US-10-981-293-24
; Sequence 24, Application US/10981293
; Publication No. US20050066390A1
; GENERAL INFORMATION:
; APPLICANT: Booth, Russ
; APPLICANT: Cahoon, Rebecca E
; APPLICANT: Hitz, William D
; APPLICANT: Kinney, Anthony
; APPLICANT: Yadav, Naren
; TITLE OF INVENTION: Nucleotide Sequences of a New Class of Diverged Delta-9 Stearoyl-
; TITLE OF INVENTION: ACP Desaturase
; FILE REFERENCE: BBI476 US NA
; CURRENT APPLICATION NUMBER: US/10/981,293
; CURRENT FILING DATE: 2004-11-04
; PRIOR APPLICATION NUMBER: US/09/934,900
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/226996
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 24
; LENGTH: 80
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: ELVISLIVES complementary
US-10-981-293-24

Query Match          51.9%; Score 80; DB 19; Length 80;
Best Local Similarity 100.0%; Pred. No. 6.3e-15;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 CGCCGAGCTGTCATCTCGCTCATCTGTCGAGTCGCGCGCCGCCGACTCGACGATGAGC 97
    |||
DB 1 CGCCGAGCTGTCATCTCGCTCATCTGTCGAGTCGCGCGCCGCCGACTCGACGATGAGC 60
```



```
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1581)
US-10-156-761-6327
```

```
Query Match
Best Local Similarity 24.7%; Score 38; DB 15; Length 1581;
Best Local Similarity 59.1%; Pred. No. 0.029;
Matches 65; Conservative 0; Mismatches 45; Indels 0; Gaps 0;
```

```
OY 42 CGAGCTGTCATCTGCTCATCTGCTGAGTGGCGCGCCGCACTGACGATGAGCGAGA 101
DB 308 CCGAGTACGTCAAGCGCGCCTCGACGCGGCGGTGACCGACGCGCCGTCGAACCGCGAG 367

OY 102 TGACCAGCTCCGCGCGCCGACTCGACGATGAGCGAGATGACCACTCCGG 151
DB 368 TCGTCGCTCCGTACTGCGACGCGCCGAGAGACCCGCGAAGTGTCTCGG 417
```

RESULT 36

```
US-10-156-761-6327/c
; Sequence 6327, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 6327
; LENGTH: 1581
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1581)
US-10-156-761-6327
```

```
Query Match
Best Local Similarity 24.7%; Score 38; DB 15; Length 1581;
Best Local Similarity 59.1%; Pred. No. 0.029;
Matches 65; Conservative 0; Mismatches 45; Indels 0; Gaps 0;
```

```
OY 4 CCGAGCTGTCATCTGCTCATCTGCTGAGTGGCGCGCCGCACTGTCATCTGCTCAT 63
DB 417 CCGAGCAGTTCGCGCGGCTCGTCCGCGCTCGCAGTACGAGGCGGACGACCTCGCGGT 358

OY 64 CGTCGAGTCCGCGCGCGCCGCACTCGACGATGAGCGAGATGACCACTCCG 113
DB 357 CGACGGCGCGTCCGTACACGCGCGCGCTGAGGCGCGCTTGAAGTACTCGG 308
```

RESULT 37

```
US-10-156-761-1
; Sequence 1, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
```

```
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 1
; LENGTH: 9025608
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (4187715)
; OTHER INFORMATION: a, t, c, g, other or unknown
US-10-156-761-1
```

```
Query Match
Best Local Similarity 24.7%; Score 38; DB 15; Length 9025608;
Best Local Similarity 59.1%; Pred. No. 0.018;
Matches 65; Conservative 0; Mismatches 45; Indels 0; Gaps 0;
```

```
OY 42 CGAGCTGTCATCTGCTCATCTGCTGAGTGGCGCGCCGCACTGACGATGAGCGAGA 101
DB 7618751 CCGAGTACGTCAAGCGCGCCTCGACGCGGCGGTGACCGACGCGCCGTCGAACCGCGAG 7618810

OY 102 TGACCAGTCCGCGCGCCGACTCGACGATGAGCGAGATGACCACTCCGG 151
DB 7618811 TCGTCGCTCCGTACTGCGACGCGCCGAGAGACCCGCGAAGTGTCTCGG 7618860
```

RESULT 38

```
US-10-156-761-1/c
; Sequence 1, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 1
; LENGTH: 9025608
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (4187715)
; OTHER INFORMATION: a, t, c, g, other or unknown
US-10-156-761-1
```

```
Query Match
Best Local Similarity 24.7%; Score 38; DB 15; Length 9025608;
Best Local Similarity 59.1%; Pred. No. 0.018;
Matches 65; Conservative 0; Mismatches 45; Indels 0; Gaps 0;
```

```
OY 4 CCGAGCTGTCATCTGCTCATCTGCTGAGTGGCGCGCCGCACTGTCATCTGCTCAT 63
DB 7618860 CCGAGCAGTTCGCGCGGCTCGTCCGCGCTCGCAGTACGAGGCGAGCACTCGCGGT 7618801
```


; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 51952
; LENGTH: 742
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_54296C.1
US-10-437-963-51952

Query Match 23.6%; Score 36.4; DB 18; Length 742;
Best Local Similarity 58.2%; Pred. No. 0.093;
Matches 64; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

QY 4 CCGAGCTGTCATCTCGCTCATCTCGAGTCGGCGCGGAGCTGTCATCTCGTCAT 63
DB 282 CCGAGGTCGTCGTCGCGCGCGCGCGGACCGGAGTCGACCGGAGAGCTGTGCTCT 223
QY 64 CGTCGAGTCGGCGCGCGCGGACTCGACGATGAGCGAGATGACCACTCCG 113
DB 222 CATCGAGCGCGCGCGGAGGAGCGGACGACGACCGGGTAGCCGGAACGCGG 173

RESULT 43

US-10-437-963-85043
; Sequence 85043, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 85043
; LENGTH: 561
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_8421C.1
US-10-437-963-85043

Query Match 23.4%; Score 36; DB 18; Length 561;
Best Local Similarity 54.5%; Pred. No. 0.13;
Matches 72; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 18 CTGCTCATCTCGAGTCGGCGCGGAGCTGTGTCATCTCGCTCATCTCGAGTCGGCGG 77
DB 87 CTGATCATGATGATCACCAGGTCGACACCGGTGTCGCTGCGCTGCTCTCTCGCGG 146
QY 78 CCGCCGACTCGAGTCGATGAGCGGAGATGACCACTCCGCGCGGACTCGACGATGAGCGAG 137
DB 147 CCGCCGCGCTCGCCACCAAGACGACGGTCTCCGGTACCGTCCGATCAACATGACG 206
QY 138 ATGACCACTCC 149
DB 207 ACGACCAACACC 218

RESULT 44

US-10-437-963-85043/c

; Sequence 85043, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 85043
; LENGTH: 561
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_8421C.1
US-10-437-963-85043

Query Match 23.4%; Score 36; DB 18; Length 561;
Best Local Similarity 54.5%; Pred. No. 0.13;
Matches 72; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 6 GGAGCTGTCATCTCGCTCATCTCGAGTCGGCGCGGAGCTGTCATCTCGTCATCG 65
DB 218 GGTGTCGTCGTCGTCATGTCATCGGACCGGTAGCCGAGACCGTCTTGCGTGGCG 159
QY 66 TCGAGTCGGCGCGCGCGGACTCGACGATGAGCGGAGATGACCACTCCGCGCGGACTCG 125
DB 158 AGCGCGCGCGCGCGGAGGAGGAGCGGACCGGAGGACCGGTCGACCTGTGATCA 99
QY 126 ACGATGAGCGAG 137
DB 98 TCACTGATGACG 87

RESULT 45

US-10-437-963-36912
; Sequence 36912, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 36912
; LENGTH: 816
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_40691C.1
US-10-437-963-36912

Query Match 23.4%; Score 36; DB 18; Length 816;
Best Local Similarity 55.6%; Pred. No. 0.12;
Matches 69; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

Qy	31	GATCGGCGCGCGAGCTGTGTCATCTGCTCATCGTGGAGTGGCGCGCGCGACTGAC	90
Db	418	GAGCGCGAGCAGGATCCGCGCGCTTCACCATGACTCGTGGCGCGCGCGCGCAC	477
Qy	91	GATGAGCGAGATGACCAGCTCCGCGCGCGACTCGACGATGAGCGAGATGACCAGCTCCG	150
Db	478	CACCACCAACCAACAGACGCGCGCGCGCGCACCTCCGGCACCACTACTCAGCCCC	537
Qy	151	GCCG 154	
Db	538	GCCG 541	

Search completed: April 9, 2005, 01:03:46
Job time : 528 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 8, 2005, 21:38:34 ; Search time 434 Seconds
(without alignments)
2100.553 Million cell updates/sec

Title: US-09-887-194A-13

Perfect score: 154

Sequence: 1 cggcgcgagctgtcatctc.....gagatgaccagctccgccc 154

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 100 summaries

Database : N_Geneseq_16Dec04:*

- 1: geneseqn1980s:*
- 2: geneseqn1990s:*
- 3: geneseqn2000s:*
- 4: geneseqn2001as:*
- 5: geneseqn2001bs:*
- 6: geneseqn2002as:*
- 7: geneseqn2002bs:*
- 8: geneseqn2003as:*
- 9: geneseqn2003bs:*
- 10: geneseqn2003cs:*
- 11: geneseqn2003ds:*
- 12: geneseqn2004as:*
- 13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	154	100.0	154	6	AAD29231 Plasmids
2	154	100.0	154	6	AAD29231 Plasmids
3	154	100.0	154	6	AAD32908 Plasmid p
4	154	100.0	154	6	AAD32908 Plasmid p
5	154	100.0	154	12	ADQ07968 Seed spec
6	154	100.0	154	12	ADQ07968 Seed spec
7	154	100.0	7701	12	ADP89887 Seed-spec
8	154	100.0	7701	12	ADP89887 Seed-spec
9	154	100.0	7701	12	ADP67892 Seed-spec
10	154	100.0	7701	12	ADP67892 Seed-spec
11	154	100.0	7701	12	ADQ07962 Seed spec
12	154	100.0	7701	12	ADQ07962 Seed spec
13	112	72.7	4974	6	ABK10072 Plasmid p
14	112	72.7	4974	6	ABK10072 Plasmid p
15	82.8	53.8	6611	6	AAD32909 PBS68 pla
16	82.8	53.8	6611	6	AAD32909 PBS68 pla
17	81	52.6	81	6	ABK10711 Artificialia
18	81	52.6	81	6	ABK10711 Artificialia
19	81	52.6	963	6	AAD29247 Plasmid p
20	81	52.6	963	6	AAD29247 Plasmid p

21	80	51.9	80	6	AAD29230	Aad29230 Plasmids
22	80	51.9	80	6	AAD29230	Aad29230 Plasmids
23	80	51.9	80	6	AAD32907	Aad32907 Plasmids
24	80	51.9	80	6	AAD32907	Aad32907 Plasmids
25	80	51.9	92	6	ABK10712	Abk10712 Artificialia
26	80	51.9	92	6	ABK10712	Abk10712 Artificialia
27	80	51.9	92	6	AAD29232	Aad29232 ELVISLIVE
28	80	51.9	92	6	AAD29232	Aad29232 ELVISLIVE
29	45.8	29.7	1717	6	AAD29242	Aad29242 Plasmid p
30	45.8	29.7	1717	6	AAD29242	Aad29242 Plasmid p
31	44	28.6	44	6	ABK10710	Abk10710 Artificialia
32	44	28.6	44	6	ABK10710	Abk10710 Artificialia
33	38.2	24.8	1251	13	AD514722	Ad514722 Pseudomon
34	38.2	24.8	1251	13	AD514722	Ad514722 Pseudomon
35	35.2	22.9	2730	12	ADJ40055	Adj40055 Plant CDN
36	35.2	22.9	2730	12	ADJ40055	Adj40055 Plant CDN
37	35	22.7	850	12	ACH91679	Ach91679 Human gen
38	35	22.7	850	12	ACH91679	Ach91679 Human gen
39	35	22.7	1797	13	ADP24630	Adp24630 PRO polyp
40	35	22.7	1797	13	ADP24630	Adp24630 PRO polyp
41	34.8	22.6	1681	6	AA518438	Aas18438 Contig 11
42	34.8	22.6	1681	6	AA518438	Aas18438 Contig 11
43	34.8	22.6	1681	12	ADJ1894	AdJ1894 Streptomy
44	34.8	22.6	1681	12	ADJ1894	AdJ1894 Streptomy
45	34.6	22.5	1498	4	AA559803	Aas59803 Propionib
46	34.6	22.5	1498	4	AA559803	Aas59803 Propionib
47	34.6	22.5	1498	8	ACF64732	Acf64732 Propionib
48	34.6	22.5	1498	8	ACF64732	Acf64732 Propionib
49	34.6	22.5	6422	4	AA559655	Aas59655 Propionib
50	34.6	22.5	6422	4	AA559655	Aas59655 Propionib
51	34.6	22.5	6422	8	ACF64584	Acf64584 Propionib
52	34.6	22.5	6422	8	ACF64584	Acf64584 Propionib
53	34.2	22.2	1245	12	ADJ42694	Adj42694 Plant CDN
54	34.2	22.2	1245	12	ADJ42694	Adj42694 Plant CDN
55	34	22.1	110000	4	AA199682_42	Continuation (43 o
56	34	22.1	110000	4	AA199682_42	Continuation (43 o
57	34	22.1	110000	4	AA199683_42	Continuation (43 o
58	34	22.1	110000	4	AA199683_42	Continuation (43 o
59	33.8	21.9	1269	8	ADA70222	Ada70222 Rice gene
60	33.8	21.9	1269	8	ADA70222	Ada70222 Rice gene
61	33.8	21.9	1386	10	ADB62908	Adb62908 Human CDN
62	33.8	21.9	1386	10	ADB62908	Adb62908 Human CDN
63	33.8	21.9	2821	4	AA166075	Aai66075 Triticum
64	33.6	21.8	2821	4	AA166075	Aai66075 Triticum
65	33.6	21.8	1233	8	ACA38203	Aca38203 Prokaryot
66	33.6	21.8	1233	8	ACA38203	Aca38203 Prokaryot
67	33.4	21.7	747	11	ABD05813	Abd05813 Pseudomon
68	33.4	21.7	747	11	ABD05813	Abd05813 Pseudomon
69	33.4	21.7	1105	8	ACA23458	Aca23458 Prokaryot
70	33.4	21.7	1105	8	ACA23458	Aca23458 Prokaryot
71	33.4	21.7	1796	10	ACC72814	Acc72814 Human can
72	33.4	21.7	1796	10	ACC72814	Acc72814 Human can
73	33.4	21.7	1796	11	ADN39742	Adn39742 Cancer/an
74	33.4	21.7	1796	11	ADN39742	Adn39742 Cancer/an
75	33.4	21.7	3225	11	ABD06018	Abd06018 Pseudomon
76	33.4	21.7	3225	11	ABD06018	Abd06018 Pseudomon
77	33.2	21.6	722	12	ADI42872	Adi42872 Plant tra
78	33.2	21.6	722	12	ADI42872	Adi42872 Plant tra
79	33.2	21.6	1575	4	AA60762	Aaf60762 Pseudomona
80	33.2	21.6	1575	4	AA60762	Aaf60762 Pseudomona
81	33.2	21.6	2307	8	ACA26151	Aca26151 Prokaryot
82	33.2	21.6	2307	8	ACA26151	Aca26151 Prokaryot
83	33	21.4	345	3	AA604565	Aac04565 Human sec
84	33	21.4	345	3	AA604565	Aac04565 Human sec
85	32.8	21.3	9210	4	AAH52046	Aah52046 Mycobacte
86	32.8	21.3	9210	4	AAH52046	Aah52046 Mycobacte
87	32.8	21.3	32329	12	AD051695	Ad051695 Streptomy
88	32.8	21.3	32329	12	AD051695	Ad051695 Streptomy
89	32.8	21.3	110000	4	AA199682_28	Continuation (29 o
90	32.8	21.3	110000	4	AA199682_28	Continuation (29 o
91	32.8	21.3	110000	4	AA199683_28	Continuation (29 o
92	32.8	21.3	110000	4	AA199683_28	Continuation (29 o
93	32.4	21.0	2034	12	ADJ44932	Adj44932 Plant CDN

c	94	32.4	21.0	2034	12	ADJ44932	Adj44932 Plant CDN
c	95	32.4	21.0	2237	2	AAQ89779	Aaq89779 Cotranspo
c	96	32.4	21.0	2237	2	AAQ89779	Aaq89779 Cotranspo
c	97	32.4	21.0	135638	10	ABX34289	Abx34289 S. atrool
c	98	32.4	21.0	135638	10	ABX34289	Abx34289 S. atrool
c	99	32.2	20.9	441	12	ADJ44648	Adj44648 Plant CDN
c	100	32.2	20.9	441	12	ADJ44648	Adj44648 Plant CDN

ALIGNMENTS

```
RESULT 1
AAD29231
ID  AAD29231 standard; DNA; 154 BP.
XX
AC  AAD29231;
XX
DT  07-MAY-2002 (first entry)
XX
DE  Plasmids pKS133 2X ELVISLIVES complementary repeat DNA.
XX
KM  Recombinant construct; gene expression; plasmid pKS133; ds.
XX
OS  Unidentified.
XX
FH  Key Location/Qualifiers
FT  CDS 7..36
FT  /*tag= a
FT  /product= "ELVISLIVES protein"
FT  CDS 44..74
FT  /*tag= b
FT  /product= "ELVISLIVES protein"
FT  CDS complement(82..111)
FT  /*tag= c
FT  /product= "ELVISLIVES protein"
FT  CDS complement(119..148)
FT  /*tag= d
FT  /product= "ELVISLIVES protein"
XX
PN  WO200200904-A2.
XX
PD  03-JAN-2002.
XX
PF  22-JUN-2001; 2001WO-US019962.
XX
PR  23-JUN-2000; 2000US-0213961P.
XX
PA  (DUPO ) DU PONT DE NEMOURS & CO E I.
XX  (PION-) PIONEER HI-BRED INT INC.
XX
PI  Glassman KF, Gordon-Kamm WJ, Kinney AJ, Lowe K, Stecca KL;
PI  Nichols SE;
XX
DR  WPI; 2002-139927/18.
DR  P-PSDB; AAE18333.
XX
XX  New recombinant construct having a promoter operably linked to a DNA
PT  sequence which when expressed produces an RNA having homology to a target
PT  mRNA and its reverse complement unrelated to endogenous DNA, for reducing
PT  gene expression.
XX
PS  Claim 45; Page 37; 77pp; English.
XX
CC  The present invention relates to a new recombinant construct. The
CC  construct comprises a promoter operably linked to a DNA sequence which
CC  when expressed by a host produces an RNA having homology to at least one
CC  target mRNA expressed by the host and complementary RNA regions. The
CC  recombinant construct is useful for reducing the expression of a target
CC  mRNA or any similar endogenous mRNA. The RNAs expressed from the
CC  recombinant constructs are also used in reducing expression of a target
CC  mRNA or any similar endogenous mRNA. The sequences and their reverse
CC  complements can be used to reduce the expression of any endogenous
```

CC genomic sequence that shares substantial similarity to nucleic acid
CC fragment which is in proximity to the DNA or RNA sequence derived from
CC it. The present sequence is 2X ELVISLIVES complementary repeat region DNA
CC found in plasmid pKS133 used in the exemplification of the invention

SQ Sequence 154 BP; 24 A; 53 C; 53 G; 24 T; 0 U; 0 Other;

Query Match 100.0%; Score 154; DB 6; Length 154;
Best Local Similarity 100.0%; Pred. No. 2.7e-28;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 CGGCCGAGCTGGTCACTCTCGCTCATCGAGTCGGCGCGCGAGCTGTCATCTGCT 60
Db 1 CGGCCGAGCTGGTCACTCTCGCTCATCGAGTCGGCGCGCGAGCTGTCATCTGCT 60
QY 61 CATCGTCGAGTCGGCGCGCGCGCGACTCGACGATGAGCGAGATGACCACTCCGCGCG 120
Db 61 CATCGTCGAGTCGGCGCGCGCGCGACTCGACGATGAGCGAGATGACCACTCCGCGCG 120
QY 121 ACTGACGATGAGCGGAGATGACCACTCCGCGCG 154
Db 121 ACTGACGATGAGCGGAGATGACCACTCCGCGCG 154
```

RESULT 2

```
AAD29231/c
ID  AAD29231 standard; DNA; 154 BP.
XX
AC  AAD29231;
XX
DT  07-MAY-2002 (first entry)
XX
DE  Plasmids pKS133 2X ELVISLIVES complementary repeat DNA.
XX
KM  Recombinant construct; gene expression; plasmid pKS133; ds.
XX
OS  Unidentified.
XX
FH  Key Location/Qualifiers
FT  CDS 7..36
FT  /*tag= a
FT  /product= "ELVISLIVES protein"
FT  CDS 44..74
FT  /*tag= b
FT  /product= "ELVISLIVES protein"
FT  CDS complement(82..111)
FT  /*tag= c
FT  /product= "ELVISLIVES protein"
FT  CDS complement(119..148)
FT  /*tag= d
FT  /product= "ELVISLIVES protein"
XX
PN  WO200200904-A2.
XX
PD  03-JAN-2002.
XX
PF  22-JUN-2001; 2001WO-US019962.
XX
PR  23-JUN-2000; 2000US-0213961P.
XX
PA  (DUPO ) DU PONT DE NEMOURS & CO E I.
XX  (PION-) PIONEER HI-BRED INT INC.
XX
PI  Glassman KF, Gordon-Kamm WJ, Kinney AJ, Lowe K, Stecca KL;
PI  Nichols SE;
XX
DR  WPI; 2002-139927/18.
DR  P-PSDB; AAE18333.
XX
XX  New recombinant construct having a promoter operably linked to a DNA
PT  sequence which when expressed produces an RNA having homology to a target
PT  mRNA and its reverse complement unrelated to endogenous DNA, for reducing
PT  gene expression.
```

XX Claim 45; Page 37; 77pp; English.

PS The present invention relates to a new recombinant construct. The

XX construct comprises a promoter operably linked to a DNA sequence which

CC when expressed by a host produces an RNA having homology to at least one

CC target mRNA expressed by the host and complementary RNA regions. The

CC recombinant construct is useful for reducing the expression of a target

CC mRNA or any similar endogenous mRNA. The RNAs expressed from the

CC recombinant constructs are also used in reducing expression of a target

CC mRNA or any similar endogenous mRNA. The sequences and their reverse

CC complements can be used to reduce the expression of any endogenous

CC genomic sequence that shares substantial similarity to nucleic acid

CC fragment which is in proximity to the DNA or RNA sequence derived from

CC it. The present sequence is 2X ELVISLIVES complementary repeat region DNA

CC found in plasmid pKS133 used in the exemplification of the invention

XX

SQ Sequence 154 BP; 24 A; 53 C; 53 G; 24 T; 0 U; 0 Other;

Query Match 100.0%; Score 154; DB 6; Length 154;

Best Local Similarity 100.0%; Pred. No. 2.7e-28;

Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CGGCCGAGCTGGTCATCTCGCTCATCTGAGTCGGCGCGGAGCTGTCTATCTCGCT 60

DB 154 CGGCCGAGCTGGTCATCTCGCTCATCTGAGTCGGCGCGGAGCTGTCTATCTCGCT 95

OY 61 CATCGTCGAGTCGGCGCGCGCGGAGCTGACGATGAGCGAGATGACCACTCCGGCCGCG 120

DB 94 CATCGTCGAGTCGGCGCGCGCGGAGCTGACGATGAGCGAGATGACCACTCCGGCCGCG 35

OY 121 ACTCGACGATGAGCGAGATGACCACTCCGGCCG 154

DB 34 ACTCGACGATGAGCGAGATGACCACTCCGGCCG 1

RESULT 3

AAD32908 standard; DNA; 154 BP.

XX ID AAD32908;

AC AAD32908;

XX

DT 01-JUL-2002 (first entry)

XX

DE Plasmid pKS133 2X ELVISLIVES complementary repeat DNA.

XX

KM Rice; diverged delta-9 fatty acid desaturase; enzyme; cellular lipid;

KW oil; transgenic plant; gene mapping; immunisation; plasmid pKS133; gene;

KW ds.

XX

OS Unidentified.

XX

XX Key Location/Qualifiers

FT 7..36

FT CDS /product= "ELVISLIVES protein"

FT 44..74

FT CDS /product= "ELVISLIVES protein"

FT complement(82..111)

FT /tag= c

FT /product= "ELVISLIVES protein"

FT complement(119..148)

FT /tag= d

FT /product= "ELVISLIVES protein"

XX

PN WO200216565-A2.

XX

PD 28-FEB-2002.

XX

XX 22-AUG-2001; 2001WO-US026246.

PF 22-AUG-2000; 2000US-0226996P.

XX

XX (DUPO) DU PONT DE NEMOURS & CO E I.

PA Booth JR, Cahoon RE, Hitz WD, Kinney AJ, Yadav NS;

XX WPI; 2002-269353/31.

DR P-PSDB; AAE20554.

XX

PT New delta-9 fatty acid desaturase polypeptides and polynucleotides,

PT useful in creating transgenic plants having altered levels of mono-, poly

PT - and unsaturated fatty acids and in increasing the unsaturation levels

PT in cellular lipids.

XX

PS Example 9; Page 43; 77pp; English.

XX

CC The present invention relates to diverged delta-9 fatty acid desaturase

CC proteins and polynucleotides encoding such proteins. The nucleic acid

CC sequences may be used to increase the level of unsaturation in cellular

CC lipids, including oil, in tissues when the enzyme is absent or rate-

CC limiting, to isolate cDNAs and genes encoding homologous proteins from

CC the same or other plant species and to create transgenic plants in which

CC the polypeptides are present at higher or lower levels than normal or in

CC cell types or developmental stages in which they are not normally found,

CC thus altering the level of mono-, poly- and unsaturated fatty acids in

CC those cells. They are useful as probes for genetic and physical gene

CC mapping and as markers, e.g. restriction fragment length polymorphism

CC (RFLP) markers. The peptides can be used to immunise animals to produce

CC antibodies specific for the peptides and proteins. The present sequence

CC is 1X ELVISLIVES complementary repeat region DNA found in plasmid pKS133

CC This sequence is used in the exemplification of the invention for the

CC suppression of Fad2 in soybean

XX

SQ Sequence 154 BP; 24 A; 53 C; 53 G; 24 T; 0 U; 0 Other;

Query Match 100.0%; Score 154; DB 6; Length 154;

Best Local Similarity 100.0%; Pred. No. 2.7e-28;

Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CGGCCGAGCTGGTCATCTCGCTCATCTGAGTCGGCGCGGAGCTGTCTATCTCGCT 60

DB 1 CGGCCGAGCTGGTCATCTCGCTCATCTGAGTCGGCGCGGAGCTGTCTATCTCGCT 60

OY 61 CATCGTCGAGTCGGCGCGCGCGGAGCTGACGATGAGCGAGATGACCACTCCGGCCGCG 120

DB 61 CATCGTCGAGTCGGCGCGCGCGGAGCTGACGATGAGCGAGATGACCACTCCGGCCGCG 120

OY 121 ACTCGACGATGAGCGAGATGACCACTCCGGCCG 154

DB 121 ACTCGACGATGAGCGAGATGACCACTCCGGCCG 154

RESULT 4

AAD32908/c

XX ID AAD32908 standard; DNA; 154 BP.

XX

AC AAD32908;

XX

DT 01-JUL-2002 (first entry)

XX

DE Plasmid pKS133 2X ELVISLIVES complementary repeat DNA.

XX

KM Rice; diverged delta-9 fatty acid desaturase; enzyme; cellular lipid;

KW oil; transgenic plant; gene mapping; immunisation; plasmid pKS133; gene;

KW ds.

XX

OS Unidentified.

XX

XX Key Location/Qualifiers

FT 7..36

FT CDS /product= "ELVISLIVES protein"

FT 44..74

FT CDS /product= "ELVISLIVES protein"

FT /tag= b

FT /product= "ELVISLIVES protein"
FT complement(82. .111)
FT /*tag= c
FT /product= "ELVISLIVES protein"
FT complement(119. .148)
FT /*tag= d
FT /product= "ELVISLIVES protein"
XX
PN WO200216565-A2.
XX
PD 28-FEB-2002.
XX
PF 22-AUG-2001; 2001WO-US026246.
XX
PR 22-AUG-2000; 2000US-0226996P.
XX
PA (DUPO) DU PONT DE NEMOURS & CO E I.
XX
PI Booth JR, Cahoon RE, Hiltz WD, Kinney AJ, Yadav NS;
XX
DR WPI; 2002-269353/31.
DR P-PSDB; AAE20554.
XX
XX New delta-9 fatty acid desaturase polypeptides and polynucleotides,
PT useful in creating transgenic plants having altered levels of mono-, poly
PT - and unsaturated fatty acids and in increasing the unsaturation levels
PT in cellular lipids.
XX
PS Example 9; Page 43; 77pp; English.
XX
CC The present invention relates to diverged delta-9 fatty acid desaturase
CC proteins and polynucleotides encoding such proteins. The nucleic acid
CC sequences may be used to increase the level of unsaturation in cellular
CC lipids, including oil, in tissues when the enzyme is absent or rate-
CC limiting, to isolate cDNAs and genes encoding homologous proteins from
CC the same or other plant species and to create transgenic plants in which
CC the polypeptides are present at higher or lower levels than normal or in
CC cell types or developmental stages in which they are not normally found,
CC thus altering the level of mono-, poly- and unsaturated fatty acids in
CC those cells. They are useful as probes for genetic and physical gene
CC mapping and as markers, e.g. restriction fragment length polymorphism
CC (RFLP) markers. The peptides can be used to immunise animals to produce
CC antibodies specific for the peptides and proteins. The present sequence
CC is 1X ELVISLIVES complementary repeat region DNA found in plasmid PKS133
CC This sequence is used in the exemplification of the invention for the
CC suppression of Fad2 in soybean
XX
SQ Sequence 154 BP; 24 A; 53 C; 53 G; 24 T; 0 U; 0 Other;
Query Match 100.0%; Score 154; DB 6; Length 154;
Best Local Similarity 100.0%; Pred. No. 2.7e-28;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGGCCGAGCTGGTCATCTCGCTCATCTCGAGTCGGCGCGGAGCTGTGTCATCTCGCT 60
DB 154 CGGCCGAGCTGGTCATCTCGCTCATCTCGAGTCGGCGCGGAGCTGTGTCATCTCGCT 95
QY 61 CATCGTCGAGTCGGCGCGCGCGGAGCTGACGATGAGCGAGATGACCACTCCGCGCGCG 120
DB 94 CATCGTCGAGTCGGCGCGCGCGGAGCTGACGATGAGCGAGATGACCACTCCGCGCGCG 35
QY 121 ACTGACGATGAGCGAGATGACCACTCCGCGCG 154
DB 34 ACTGACGATGAGCGAGATGACCACTCCGCGCG 1

XX
DE Seed specific gene silencing vector PKS151, stem loop region.
XX
KW PKS151; seed specific promoter; gene silencing; chalcone reductase;
KW transgenic; liquiritigenin-derived isoflavone; isoflavonoid;
KW food product; snack food product; baked good product; fried food product;
KW health food product; infant formula; beverage; nutritional supplement;
KW dairy product; pet food product; animal feed; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT stem_loop 1..154
FT /*tag= a
XX
PN US2004128714-A1.
XX
PD 01-JUL-2004.
XX
PF 11-DEC-2003; 2003US-00734947.
XX
PR 13-DEC-2002; 2002US-0433433P.
XX
PA (MCGO/) MCGONIGLE B.
XX
PI Mgonigle B;
XX
DR WPI; 2004-533136/51.
XX
PT Decreasing ratio of liquiritigenin-derived isoflavones relative to total
PT isoflavones in a plant comprises transforming plant cell with nucleic
PT acid sequence showing homology to sequence encoding chalcone reductase
PT (deoxychalcone synthase).
XX
PS Example 7; SEQ ID NO 7; 25pp; English.
XX
CC The invention relates to decreasing the ratio of liquiritigenin-derived
CC isoflavones relative to the total isoflavones in an isoflavonoid-
CC producing plant comprising transforming a plant cell with a recombinant
CC construct comprising a promoter operably linked to a nucleic acid
CC sequence of at least 200 nucleotides having at least 75% sequence
CC identity to ADQ07965 (a soybean chalcone reductase cDNA). Also included
CC are an isoflavonoid-producing plant made by the method above, seeds or
CC plant parts of the plant, an isoflavonoid-containing protein product
CC having a reduced ratio of liquiritigenin-derived isoflavones relative to
CC the total isoflavone levels obtained from the seeds or plant parts, a
CC food (or a nutritional supplement, a food bar, or a beverage) which has
CC incorporated the isoflavonoid-containing product, and a method of
CC producing an isoflavonoid-containing product having a reduced ratio of
CC liquiritigenin-derived isoflavones relative to the total isoflavone
CC levels. The recombinant construct comprises a stem-loop structure. The
CC nucleic acid sequence forms a loop in the stem-loop structure and the
CC stem comprises a sequence of ADQ07968). The promoter is a seed-specific
CC promoter. The method is useful for decreasing the ratio of liquiritigenin
CC -derived isoflavones relative to the total isoflavones in an isoflavone-
CC producing plant. The methods and recombinant construct are useful in
CC producing an isoflavonoid-containing product which is incorporated in
CC cereal food product, snack food product, baked good product, fried food
CC product, health food product, infant formula, beverage, nutritional
CC supplement, dairy product, pet food product, or animal feed. The present
CC sequence is the single stranded version of the stem loop region from
CC plasmid PKS151.
XX
SQ Sequence 154 BP; 24 A; 53 C; 53 G; 24 T; 0 U; 0 Other;
Query Match 100.0%; Score 154; DB 12; Length 154;
Best Local Similarity 100.0%; Pred. No. 2.7e-28;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGGCCGAGCTGGTCATCTCGCTCATCTCGAGTCGGCGCGGAGCTGTGTCATCTCGCT 60
DB 1 CGGCCGAGCTGGTCATCTCGCTCATCTCGAGTCGGCGCGGAGCTGTGTCATCTCGCT 60

OY 61 CATCGTCGAGTCGGCGCCGCCGACTCGACGATGAGCGAGATGACCACTCCGCCGCCCG 120
|||||
DB 61 CATCGTCGAGTCGGCGCCGCCGACTCGACGATGAGCGAGATGACCACTCCGCCGCCCG 120
OY 121 ACTCGACGATGAGCGAGATGACCACTCCGCCCG 154
|||||
DB 121 ACTCGACGATGAGCGAGATGACCACTCCGCCCG 154
RESULT 6
ADQ07968/c
ID ADQ07968 standard; DNA; 154 BP.
XX
AC ADQ07968;
XX
DT 23-SEP-2004 (first entry)
XX
DE Seed specific gene silencing vector pKS151, stem loop region.
XX
KW pKS151; seed specific promoter; gene silencing; chalcone reductase;
KW transgenic; liquiritigenin-derived isoflavone; isoflavonoid;
KW food product; snack food product; baked good product; fried food product;
KW health food product; infant formula; beverage; nutritional supplement;
KW dairy product; pet food product; animal feed; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT stem_loop 1..154
FT /*tag= a
XX
PN US2004128714-A1.
XX
PD 01-JUL-2004.
XX
PF 11-DEC-2003; 2003US-00734947.
XX
PR 13-DEC-2002; 2002US-0433433P.
XX
PA (MCGO/) MCGONIGLE B.
XX
PI Mgonigle B;
XX
DR WPI; 2004-533136/51.
XX
PT Decreasing ratio of liquiritigenin-derived isoflavones relative to total
PT isoflavones in a plant comprises transforming plant cell with nucleic
PT acid sequence showing homology to sequence encoding chalcone reductase
PT (deoxychalcone synthase).
XX
PS Example 7; SEQ ID NO 7; 25pp; English.
XX
CC The invention relates to decreasing the ratio of liquiritigenin-derived
CC isoflavones relative to the total isoflavones in an isoflavonoid-
CC producing plant comprising transforming a plant cell with a recombinant
CC construct comprising a promoter operably linked to a nucleic acid
CC sequence of at least 200 nucleotides having at least 75% sequence
CC identity to ADQ07965 (a soybean chalcone reductase cDNA). Also included
CC are an isoflavonoid-producing plant made by the method above, seeds or
CC plant parts of the plant, an isoflavonoid-containing protein product
CC having a reduced ratio of liquiritigenin-derived isoflavones relative to
CC the total isoflavone levels obtained from the seeds or plant parts, a
CC food (or a nutritional supplement, a food bar, or a beverage) which has
CC incorporated the isoflavonoid-containing product, and a method of
CC producing an isoflavonoid-containing product having a reduced ratio of
CC liquiritigenin-derived isoflavones relative to the total isoflavone
CC levels. The recombinant construct comprises a stem-loop structure. The
CC nucleic acid sequence forms a loop in the stem-loop structure and the
CC stem comprises a sequence of ADQ07968). The promoter is a seed-specific
CC promoter. The method is useful for decreasing the ratio of liquiritigenin
CC -derived isoflavones relative to the total isoflavones in an isoflavone-
CC producing plant. The methods and recombinant construct are useful in
CC producing an isoflavonoid-containing product which is incorporated in

CC cereal food product, snack food product, baked good product, fried food
CC product, health food product, infant formula, beverage, nutritional
CC supplement, dairy product, pet food product, or animal feed. The present
CC sequence is the single stranded version of the stem loop region from
CC plasmid pKS151.
XX
SQ Sequence 154 BP; 24 A; 53 C; 53 G; 24 T; 0 U; 0 Other;
Query Match 100.0%; Score 154; DB 12; Length 154;
Best Local Similarity 100.0%; Pred. No. 2.7e-28;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 CGGCCGAGCTGCTCATCTCGCTCATCGAGTCGGCGCCGAGAGCTGTCTATCTCGCT 60
|||||
DB 154 CGGCCGAGCTGCTCATCTCGCTCATCGAGTCGGCGCCGAGAGCTGTCTATCTCGCT 95
OY 61 CATCGTCGAGTCGGCGCCGCCGACTCGACGATGAGCGAGATGACCACTCCGCCGCCCG 120
|||||
DB 94 CATCGTCGAGTCGGCGCCGCCGACTCGACGATGAGCGAGATGACCACTCCGCCGCCCG 35
OY 121 ACTCGACGATGAGCGAGATGACCACTCCGCCCG 154
|||||
DB 34 ACTCGACGATGAGCGAGATGACCACTCCGCCCG 1
RESULT 7
ADF89887
ID ADF89887 standard; DNA; 7701 BP.
XX
AC ADF89887;
XX
DT 26-FEB-2004 (first entry)
XX
DE Seed-specific expression vector pKS151 nucleotide sequence.
XX
KW Oxidosqualene cyclase; triterpene; plant protectant; industrial product;
KW plant; soybean; beta-amyrin synthase; ds.
XX
OS Synthetic.
XX
PN WO2003095615-A2.
XX
PD 20-NOV-2003.
XX
PF 05-MAY-2003; 2003WO-US014218.
XX
PR 09-MAY-2002; 2002US-0379361P.
XX
PA (DUPO) DU PONT DE NEMOURS & CO E I.
XX
PI Mgonigle B, Maxwell CA, Hession AO;
XX
DR WPI; 2004-012098/01.
XX
PT New transgenic plants comprising recombinant DNA molecules encoding
PT oxidosqualene cyclase to lower triterpene level, used as feeds, foods,
PT beverages and industrial products like agricultural adjuvants or concrete
PT supplies.
XX
PS Example 1; SEQ ID NO 9; 39pp; English.
XX
CC The invention relates to a plant comprising at least one recombinant DNA
CC molecule comprising a promoter operably linked to at least a portion of
CC at least one oxidosqualene cyclase gene, the molecule sufficient to
CC suppress the production of a triterpene or any of its progeny, where the
CC progeny comprise the molecule. The oxidosqualene cyclase gene catalyzes
CC the cyclization of 2,3-oxidosqualene to form a triterpene, e.g. beta-
CC amyrin, lanosterol, lupeol, cycloartenol, alpha-amyrin, isomultifloranol
CC or any combination. The plants are useful in generating products which
CC may be used as feeds, foods, beverages and industrial products like
CC agricultural adjuvants, concrete supplies, dielectric fluids, dust
CC suppressants, fuel additives, hydraulic fluids, industrial cleaners,
CC industrial lubricants, metalworking fluids, odor reduction, paint

CC strippers, printing inks, printing supplies or saw guide oils. Saponins
CC may play a defense role against pathogens in plant tissues. The present
CC sequence represents the nucleotide sequence of a seed-specific expression
CC vector pKS151.

XX
SQ Sequence 7701 BP; 2236 A; 1702 C; 1709 G; 2053 T; 0 U; 1 Other;

Query Match 100.0%; Score 154; DB 12; Length 7701;
Best Local Similarity 100.0%; Pred. No. 3.1e-28;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGCCGAGCTGGTCACTCTCGCTCATCGTCGAGTCGGCGCCGGAGCTGTCTCATCTCGCT 60
|||
DB 5451 CGGCCGAGCTGGTCACTCTCGCTCATCGTCGAGTCGGCGCCGGAGCTGTCTCATCTCGCT 5510

QY 61 CATCGTCGAGTCGGCGCCGGCCGACTCGACGATGAGCGAGATGACCACTCCGGCCGCCG 120
|||
DB 5511 CATCGTCGAGTCGGCGCCGGCCGACTCGACGATGAGCGAGATGACCACTCCGGCCGCCG 5570

QY 121 ACTCGACGATGAGCGAGATGACCACTCCGGCCG 154
|||
DB 5571 ACTCGACGATGAGCGAGATGACCACTCCGGCCG 5604

RESULT 8

ADF89887/c
ID ADF89887 standard; DNA; 7701 BP.

XX
AC ADF89887;

DT 26-FEB-2004 (first entry)

XX
DE Seed-specific expression vector pKS151 nucleotide sequence.

XX
KM Oxidosqualene cyclase; triterpene; plant protectant; industrial product;
KM plant; soybean; beta-amyrin synthase; ds.

XX
OS Synthetic.

XX
PN WO2003095615-A2.

PD 20-NOV-2003.

PF 05-MAY-2003; 2003WO-US014218.

PR 09-MAY-2002; 2002US-0379361P.

PA (DUFO) DU PONT DE NEMOURS & CO E I.

PI Mcgonigle B, Maxwell CA, Hession AO;

DR WPI; 2004-012098/01.

XX
PT New transgenic plants comprising recombinant DNA molecules encoding
PT oxidosqualene cyclase to lower triterpene level, used as feeds, foods,
PT beverages and industrial products like agricultural adjuvants or concrete
PT supplies.

PS Example 1; SEQ ID NO 9; 39pp; English.

XX
CC The invention relates to a plant comprising at least one recombinant DNA
CC molecule comprising a promoter operably linked to at least a portion of
CC at least one oxidosqualene cyclase gene, the molecule sufficient to
CC suppress the production of a triterpene or any of its progeny, where the
CC progeny comprise the molecule. The oxidosqualene cyclase gene catalyzes
CC the cyclization of 2,3-oxidosqualene to form a triterpene, e.g. beta-
CC amyrin, lanosterol, lupeol, cycloartenol, alpha-amyrin, isomultiflorenol
CC or any combination. The plants are useful in generating products which
CC may be used as feeds, foods, beverages and industrial products like
CC agricultural adjuvants, concrete supplies, dielectric fluids, dust
CC suppressants, fuel additives, hydraulic fluids, industrial cleaners,
CC industrial lubricants, metalworking fluids, odor reduction, paint
CC strippers, printing inks, printing supplies or saw guide oils. Saponins

CC may play a defense role against pathogens in plant tissues. The present
CC sequence represents the nucleotide sequence of a seed-specific expression
CC vector pKS151.

XX
SQ Sequence 7701 BP; 2236 A; 1702 C; 1709 G; 2053 T; 0 U; 1 Other;

Query Match 100.0%; Score 154; DB 12; Length 7701;
Best Local Similarity 100.0%; Pred. No. 3.1e-28;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGCCGAGCTGGTCACTCTCGCTCATCGTCGAGTCGGCGCCGGAGCTGTCTCATCTCGCT 60
|||
DB 5604 CGGCCGAGCTGGTCACTCTCGCTCATCGTCGAGTCGGCGCCGGAGCTGTCTCATCTCGCT 5545

QY 61 CATCGTCGAGTCGGCGCCGGCCGACTCGACGATGAGCGAGATGACCACTCCGGCCGCCG 120
|||
DB 5544 CATCGTCGAGTCGGCGCCGGCCGACTCGACGATGAGCGAGATGACCACTCCGGCCGCCG 5485

QY 121 ACTCGACGATGAGCGAGATGACCACTCCGGCCG 154
|||
DB 5484 ACTCGACGATGAGCGAGATGACCACTCCGGCCG 5451

RESULT 9

ADF67892
ID ADF67892 standard; DNA; 7701 BP.

XX
AC ADF67892;

DT 11-MAR-2004 (first entry)

XX
DE Seed-specific expression vector pKS151 #SEQ ID 1.

XX
KM Isoflavonoid; transgenic plant; flavanone 3-hydroxylase; ds.

XX
OS Synthetic.

XX
PN WO2003106633-A2.

PD 24-DEC-2003.

PF 12-JUN-2003; 2003WO-US018663.

PR 13-JUN-2002; 2002US-0388280P.

PA (DUFO) DU PONT DE NEMOURS & CO E I.

PI Mcgonigle B, Odell JT;

DR WPI; 2004-062526/06.

XX
PT Increasing isoflavonoid production in an isoflavonoid-producing plant,
PT comprises transforming a plant with recombinant DNA constructs, growing
PT the transformed plant, and evaluating increased quantity of isoflavonoid.

PS Example 1; SEQ ID NO 1; 55pp; English.

XX
CC The invention relates to a method for increasing isoflavonoid production
CC in a plant, by transforming the plant with a recombinant DNA construct
CC having a polynucleotide (PN) e.g., a PN encoding all or part of flavanone
CC 3-hydroxylase, and second recombinant DNA construct having a PN encoding
CC C1 myb and a R myc-type transcription factor, growing the transformed
CC plant, and evaluating the quantity of isoflavonoid from the plant. The
CC method of the invention is useful for increasing isoflavonoid production
CC in an isoflavonoid-producing plant. The current sequence represents the
CC seed-specific expression vector pKS151, into which a polynucleotide
CC encoding a portion of soybean flavanone 3-hydroxylase was inserted in an
CC example from the invention, for the transformation of Glycine max.

XX
SQ Sequence 7701 BP; 2236 A; 1702 C; 1709 G; 2053 T; 0 U; 1 Other;

Query Match 100.0%; Score 154; DB 12; Length 7701;
Best Local Similarity 100.0%; Pred. No. 3.1e-28;

Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CGGCCGAGCTGGTCACTCTCGCTCATCGTGCAGTCCGCCGCGAGCTGTCACTCGCT 60
DB 5451 CGGCCGAGCTGGTCACTCTCGCTCATCGTGCAGTCCGCCGCGAGCTGTCACTCGCT 5510
OY 61 CATCGTCGAGTCGGCGCGCCGCGACTCGACGATGAGCGAGATGACCACTCCGGCCGCCG 120
DB 5511 CATCGTCGAGTCGGCGCGCCGCGCGACTCGACGATGAGCGAGATGACCACTCCGGCCGCCG 5570
OY 121 ACTCGACGATGAGCGAGATGACCACTCCGGCCGCCG 154
DB 5571 ACTCGACGATGAGCGAGATGACCACTCCGGCCGCCG 5604

RESULT 10

ADF67892/c
ID ADF67892 standard; DNA; 7701 BP.

XX ADF67892;

DT 11-MAR-2004 (first entry)

DE Seed-specific expression vector PKS151 #SEQ ID 1.

KW Isoflavonoid; transgenic plant; flavanone 3-hydroxylase; ds.

OS Synthetic.

PN WO2003106633-A2.

PD 24-DEC-2003.

PF 12-JUN-2003; 2003WO-US018663.

PR 13-JUN-2002; 2002US-0388280P.

PA (DUPO) DU PONT DE NEMOURS & CO E I.

PI Mcgonigle B, Odell JT;

DR WPI; 2004-062526/06.

PT Increasing isoflavonoid production in an isoflavonoid-producing plant,
PT comprises transforming a plant with recombinant DNA constructs, growing
PT the transformed plant, and evaluating increased quantity of isoflavonoid.

PS Example 1; SEQ ID NO 1; 55pp; English.

CC The invention relates to a method for increasing isoflavonoid production
CC in a plant, by transforming the plant with a recombinant DNA construct
CC having a polynucleotide (PN) e.g., a PN encoding all or part of flavanone
CC 3-hydroxylase, and second recombinant DNA construct having a PN encoding
CC C1 myb and a R myc-type transcription factor, growing the transformed
CC plant, and evaluating the quantity of isoflavonoid from the plant. The
CC method of the invention is useful for increasing isoflavonoid production
CC in an isoflavonoid-producing plant. The current sequence represents the
CC seed-specific expression vector PKS151, into which a polynucleotide
CC encoding a portion of soybean flavanone 3-hydroxylase was inserted in an
CC example from the invention, for the transformation of Glycine max.

XX Sequence 7701 BP; 2236 A; 1702 C; 1709 G; 2053 T; 0 U; 1 Other;

Query Match

Best Local Similarity 100.0%; Score 154; DB 12; Length 7701;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CGGCCGAGCTGGTCACTCTCGCTCATCGTGCAGTCCGCCGCGAGCTGTCACTCGCT 60
DB 5604 CGGCCGAGCTGGTCACTCTCGCTCATCGTGCAGTCCGCCGCGAGCTGTCACTCGCT 5545
OY 61 CATCGTCGAGTCGGCGCGCCGCGACTCGACGATGAGCGAGATGACCACTCCGGCCGCCG 120

DB 5544 CATCGTCGAGTCGGCGCGCCGCGCGACTCGACGATGAGCGAGATGACCACTCCGGCCGCCG 5485

OY 121 ACTCGACGATGAGCGAGATGACCACTCCGGCCGCCG 154
DB 5484 ACTCGACGATGAGCGAGATGACCACTCCGGCCGCCG 5451

RESULT 11

ADQ07962
ID ADQ07962 standard; DNA; 7701 BP.

XX ADQ07962;

DT 23-SEP-2004 (first entry)

DE Seed specific gene silencing vector PKS151.

KW PKS151; seed specific promoter; gene silencing; chalcone reductase;

KW transgenic; liquiritigenin-derived isoflavone; plant; soybean;

KW isoflavonoid; food product; snack food product; baked good product;

KW fried food product; health food product; infant formula; beverage;

KW nutritional supplement; dairy product; pet food product; animal feed; ds.

OS Glycine max.

OS Escherichia coli.

OS Cauliflower mosaic virus.

OS Synthetic.

FH Key Location/Qualifiers

FT CDS 5457..5486

FT /tag= a

FT /partial

FT /note= "No start or stop codon shown"

FT /product= "ELV1SLIVES peptide"

PN US2004128714-A1.

PD 01-JUL-2004.

PF 11-DEC-2003; 2003US-00734947.

PR 13-DEC-2002; 2002US-0433433P.

PA (MCGO/) MCGONIGLE B.

PI Mcgonigle B;

DR WPI; 2004-533136/51.

DR P-PSDB; ADQ07969.

XX Decreasing ratio of liquiritigenin-derived isoflavones relative to total

PT isoflavones in a plant comprises transforming plant cell with nucleic

PT acid sequence showing homology to sequence encoding chalcone reductase

PT (deoxychalcone synthase).

XX Example 1; SEQ ID NO 1; 25pp; English.

CC The invention relates to decreasing the ratio of liquiritigenin-derived
CC isoflavones relative to the total isoflavones in an isoflavonoid-
CC producing plant comprising transforming a plant cell with a recombinant
CC construct comprising a promoter operably linked to a nucleic acid
CC sequence of at least 200 nucleotides having at least 75% sequence
CC identity to ADQ07965 (a soybean chalcone reductase cDNA). Also included
CC are an isoflavonoid-producing plant made by the method above, seeds or
CC plant parts of the plant, an isoflavonoid-containing protein product
CC having a reduced ratio of liquiritigenin-derived isoflavones relative to
CC the total isoflavone levels obtained from the seeds or plant parts, a
CC food (or a nutritional supplement, a food bar, or a beverage) which has
CC incorporated the isoflavonoid-containing product, and a method of
CC producing an isoflavonoid-containing product having a reduced ratio of
CC liquiritigenin-derived isoflavones relative to the total isoflavone
CC levels. The recombinant construct comprises a stem-loop structure. The
CC nucleic acid sequence forms a loop in the stem-loop structure and the

CC stem comprises a sequence of ADQ07968). The promoter is a seed-specific
CC promoter. The method is useful for decreasing the ratio of liquiritigenin
CC -derived isoflavones relative to the total isoflavones in an isoflavone-
CC producing plant. The methods and recombinant construct are useful in
CC producing an isoflavonoid-containing product which is incorporated in
CC cereal food product, snack food product, baked good product, fried food
CC product, health food product, infant formula, beverage, nutritional
CC supplement, dairy product, pet food product, or animal feed. The present
CC sequence is the Seed specific gene silencing vector pKS151, into which
CC the soybean cDNA is cloned (into the NotI site flanked by the stem
CC regions of ADQ07968).

XX SQ Sequence 7701 BP; 2236 A; 1702 C; 1709 G; 2053 T; 0 U; 1 Other;

Query Match 100.0%; Score 154; DB 12; Length 7701;
Best Local Similarity 100.0%; Pred. No. 3.1e-28;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CGGCCGAGCTGTCATCTCGCTCATCGAGTCGGCGCGGAGCTGTCATCTCGCT 60
DB 5451 CGGCCGAGCTGTCATCTCGCTCATCGAGTCGGCGCGGAGCTGTCATCTCGCT 5510
OY 61 CATCGTCGAGTCGGCGCGCGCGCGCGAGTCGACGATGAGCGGAGATGACCACTCCGGCGCGCG 120
DB 5511 CATCGTCGAGTCGGCGCGCGCGCGCGAGTCGACGATGAGCGGAGATGACCACTCCGGCGCGCG 5570
OY 121 ACTCGACGATGAGCGAGATGACCACTCCGGCGCG 154
DB 5571 ACTCGACGATGAGCGAGATGACCACTCCGGCGCG 5604

RESULT 12
ADQ07962/c
ID ADQ07962 standard; DNA; 7701 BP.

XX AC ADQ07962;
XX DT 23-SEP-2004 (first entry)
XX DE Seed specific gene silencing vector pKS151.
XX

KM pKS151; seed specific promoter; gene silencing; chalcone reductase;
KM transgenic; liquiritigenin-derived isoflavone; plant; soybean;
KM isoflavonoid; food product; snack food product; baked good product;
KM fried food product; health food product; infant formula; beverage;
KM nutritional supplement; dairy product; pet food product; animal feed; ds.

XX Glycine max.
OS Escherichia coli.
OS Cauliflower mosaic virus.
OS Synthetic.

XX Key Location/Qualifiers
FH CDS 5457. 5486
FT /*tag= a
FT /partial
FT /note= "No start or stop codon shown"
FT /product= "ELVISLIVES peptide"

XX US2004128714-A1.

XX 01-JUL-2004.

XX 11-DEC-2003; 2003US-00734947.

XX 13-DEC-2002; 2002US-0433433P.

XX (MGO/) MCGONIGLE B.

XX Mgonigle B;

XX WPI; 2004-533136/51.

DR P-PSDB; ADQ07969.

XX Decreasing ratio of liquiritigenin-derived isoflavones relative to total
PT isoflavones in a plant comprises transforming plant cell with nucleic
PT acid sequence showing homology to sequence encoding chalcone reductase
PT (deoxychalcone synthase).

PS Example 1; SEQ ID NO 1; 25PD; English.

XX The invention relates to decreasing the ratio of liquiritigenin-derived
CC isoflavones relative to the total isoflavones in an isoflavonoid-
CC producing plant comprising transforming a plant cell with a recombinant
CC construct comprising a promoter operably linked to a nucleic acid
CC sequence of at least 200 nucleotides having at least 75% sequence
CC identity to ADQ07965 (a soybean chalcone reductase cDNA). Also included
CC are an isoflavonoid-producing plant made by the method above, seeds or
CC plant parts of the plant, an isoflavonoid-containing protein product
CC having a reduced ratio of liquiritigenin-derived isoflavones relative to
CC the total isoflavone levels obtained from the seeds or plant parts, a
CC food (or a nutritional supplement, a food bar, or a beverage) which has
CC incorporated the isoflavonoid-containing product, and a method of
CC producing an isoflavonoid-containing product having a reduced ratio of
CC liquiritigenin-derived isoflavones relative to the total isoflavone
CC levels. The recombinant construct comprises a stem-loop structure. The
CC nucleic acid sequence forms a loop in the stem-loop structure and the
CC stem comprises a sequence of ADQ07968). The promoter is a seed-specific
CC promoter. The method is useful for decreasing the ratio of liquiritigenin
CC -derived isoflavones relative to the total isoflavones in an isoflavone-
CC producing plant. The methods and recombinant construct are useful in
CC producing an isoflavonoid-containing product which is incorporated in
CC cereal food product, snack food product, baked good product, fried food
CC product, health food product, infant formula, beverage, nutritional
CC supplement, dairy product, pet food product, or animal feed. The present
CC sequence is the Seed specific gene silencing vector pKS151, into which
CC the soybean cDNA is cloned (into the NotI site flanked by the stem
CC regions of ADQ07968).

XX SQ Sequence 7701 BP; 2236 A; 1702 C; 1709 G; 2053 T; 0 U; 1 Other;

Query Match 100.0%; Score 154; DB 12; Length 7701;
Best Local Similarity 100.0%; Pred. No. 3.1e-28;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CGGCCGAGCTGTCATCTCGCTCATCGAGTCGGCGCGGAGCTGTCATCTCGCT 60
DB 5604 CGGCCGAGCTGTCATCTCGCTCATCGAGTCGGCGCGGAGCTGTCATCTCGCT 5545
OY 61 CATCGTCGAGTCGGCGCGCGCGCGAGTCGACGATGAGCGGAGATGACCACTCCGGCGCGCG 120
DB 5544 CATCGTCGAGTCGGCGCGCGCGCGAGTCGACGATGAGCGGAGATGACCACTCCGGCGCGCG 5485
OY 121 ACTCGACGATGAGCGAGATGACCACTCCGGCGCG 154
DB 5484 ACTCGACGATGAGCGAGATGACCACTCCGGCGCG 5451

RESULT 13

ABK10072
ID ABK10072 standard; DNA; 4974 BP.

XX ABK10072;

XX 05-JUN-2002 (first entry)

XX Plasmid pKS133 DNA.

XX Plasmidic phosphoglucomutase; gene; ds; plasmid pKS133.

XX Synthetic.

XX EP1174510-A2.

XX 23-JAN-2002.

XX

PF 17-JUL-2001; 2001EP-00306143.
XX
PR 17-JUL-2000; 2000US-0218712P.
XX
PA (DUPO) DU PONT DE NEMOURS & CO E I.
XX
PI Allen SM, Butler KH, Carlson TJ, Ilag LL;
XX
DR WPI; 2002-156692/21.
XX
PT Novel isolated polypeptides having phosphoglucomutase activity and
PT polynucleotides encoding the polypeptides, useful for producing
PT transgenic plants with altered plastidic phosphoglucomutase protein
PT levels.
XX
XX
PS Example 9; SEQ ID NO 17; 27pp; English.
XX
CC The invention relates to plastidic phosphoglucomutase polypeptides and
CC their related nucleic acids. The sequences are useful for producing a
CC transgenic plant, by transforming a plant cell with a polynucleotide of
CC the invention and regenerating a plant from the transformed plant cell.
CC Polynucleotide fragments are useful for suppressing the level of
CC expression of a gene encoding a polypeptide having plastidic
CC phosphoglucomutase activity. An isolated polynucleotide that affects the
CC level of expression of a plastidic phosphoglucomutase polypeptide in a
CC plant cell can be identified by introducing a DNA fragment comprising at
CC least 541 nucleotides, measuring the level of the polypeptide in the
CC plant cell containing the polynucleotide, and comparing the level of the
CC polypeptide in the plant cell containing the isolated polynucleotide with
CC the level of the polypeptide in a plant cell that does not contain the
CC isolated polynucleotide. A method for altering the level of expression of
CC a plastidic phosphoglucomutase protein in a host cell comprises
CC transforming a host cell with a chimeric gene and growing the transformed
CC cell under conditions that are suitable for expression of the chimeric
CC gene, where the expression of the gene results in production of altered
CC levels of plastidic phosphoglucomutase. This sequence represents plasmid
CC DNA used in the methods of the invention. Note: This sequence is not
CC represented in the printed specification but is based on sequence
CC information supplied by the European Patent Office
XX
SQ Sequence 4974 BP; 1444 A; 1070 C; 1003 G; 1456 T; 0 U; 1 Other;

Query Match 72.7%; Score 112; DB 6; Length 4974;
Best Local Similarity 100.0%; Pred. No. 4.5e-18;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGCCGAGCTGGTCATCTCGCTCATGTCGAGTCGGCGCCGGAGCTGTCATCTCGCT 60
DB 4863 CGGCCGAGCTGGTCATCTCGCTCATGTCGAGTCGGCGCCGGAGCTGTCATCTCGCT 4922

QY 61 CATCGTCGAGTCGGCGCCGCGCACTCGACGATGAGCGAGATGACCACTCC 112
DB 4923 CATCGTCGAGTCGGCGCCGCGCACTCGACGATGAGCGAGATGACCACTCC 4974

RESULT 14
ABK10072/c
ID ABK10072 standard; DNA; 4974 BP.
XX
AC ABK10072;
XX
DT 05-JUN-2002 (first entry)
XX
DE Plasmid pKS133 DNA.
XX
KM Plastidic phosphoglucomutase; gene; ds; plasmid pKS133.
XX
OS Synthetic.
XX
PN EP1174510-A2.
XX
PD 23-JAN-2002.
XX

PF 17-JUL-2001; 2001EP-00306143.
XX
PR 17-JUL-2000; 2000US-0218712P.
XX
PA (DUPO) DU PONT DE NEMOURS & CO E I.
XX
PI Allen SM, Butler KH, Carlson TJ, Ilag LL;
XX
DR WPI; 2002-156692/21.
XX
PT Novel isolated polypeptides having phosphoglucomutase activity and
PT polynucleotides encoding the polypeptides, useful for producing
PT transgenic plants with altered plastidic phosphoglucomutase protein
PT levels.
XX
XX
PS Example 9; SEQ ID NO 17; 27pp; English.
XX
CC The invention relates to plastidic phosphoglucomutase polypeptides and
CC their related nucleic acids. The sequences are useful for producing a
CC transgenic plant, by transforming a plant cell with a polynucleotide of
CC the invention and regenerating a plant from the transformed plant cell.
CC Polynucleotide fragments are useful for suppressing the level of
CC expression of a gene encoding a polypeptide having plastidic
CC phosphoglucomutase activity. An isolated polynucleotide that affects the
CC level of expression of a plastidic phosphoglucomutase polypeptide in a
CC plant cell can be identified by introducing a DNA fragment comprising at
CC least 541 nucleotides, measuring the level of the polypeptide in the
CC plant cell containing the polynucleotide, and comparing the level of the
CC polypeptide in the plant cell containing the isolated polynucleotide with
CC the level of the polypeptide in a plant cell that does not contain the
CC isolated polynucleotide. A method for altering the level of expression of
CC a plastidic phosphoglucomutase protein in a host cell comprises
CC transforming a host cell with a chimeric gene and growing the transformed
CC cell under conditions that are suitable for expression of the chimeric
CC gene, where the expression of the gene results in production of altered
CC levels of plastidic phosphoglucomutase. This sequence represents plasmid
CC DNA used in the methods of the invention. Note: This sequence is not
CC represented in the printed specification but is based on sequence
CC information supplied by the European Patent Office
XX
SQ Sequence 4974 BP; 1444 A; 1070 C; 1003 G; 1456 T; 0 U; 1 Other;

Query Match 72.7%; Score 112; DB 6; Length 4974;
Best Local Similarity 100.0%; Pred. No. 4.5e-18;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 43 GGAGCTGTCATCTCGCTCATGTCGAGTCGGCGCCGCCGCACTCGACGATGAGCGAGAT 102
DB 4974 GGAGCTGTCATCTCGCTCATGTCGAGTCGGCGCCGCCGCACTCGACGATGAGCGAGAT 4915

QY 103 GACCACTCCGGCCGCGCACTCGACGATGAGCGAGATGACCACTCCGGCGG 154
DB 4914 GACCACTCCGGCCGCGCACTCGACGATGAGCGAGATGACCACTCCGGCGG 4863

RESULT 15
AAD32909
ID AAD32909 standard; DNA; 6611 BP.
XX
AC AAD32909;
XX
DT 01-JUL-2002 (first entry)
XX
DE PBS68 plasmid used for diverged delta-9 desaturase suppression.
XX
KM Rice; diverged delta-9 fatty acid desaturase; enzyme; cellular lipid;
XX oil; transgenic plant; gene mapping; immunisation; plasmid PBS68; ds.
XX
OS Unidentified.
XX
XX
FH Key location/Qualifiers
FT terminator 523. .725
FT /*tag= b

XX /label= Kit3_terminator
FT misc_feature complement(880. .1920)
FT /*tag= b
FT /note= "Hygromycin selection region"
FT promoter 3260. .5348
FT /*tag= C
FT /label= Kit3_promoter
XX WO200216565-A2.
XX 28-FEB-2002.
XX
XX 22-AUG-2001; 2001WO-US026246.
XX
XX 22-AUG-2000; 2000US-0226996P.
XX
XX (DUPO) DU PONT DE NEMOURS & CO E I.
XX Booth JR, Cahoon RE, Hitz WD, Kinney AJ, Yadav NS,
XX WPI; 2002-269353/31.
XX
XX New delta-9 fatty acid desaturase polypeptides and polynucleotides,
PT useful in creating transgenic plants having altered levels of mono-, poly
PT - and unsaturated fatty acids and in increasing the unsaturation levels
PT in cellular lipids.
XX
XX Example 9; Page 76-77; 77pp; English.
XX
XX The present invention relates to diverged delta-9 fatty acid desaturase
CC proteins and polynucleotides encoding such proteins. The nucleic acid
CC sequences may be used to increase the level of unsaturation in cellular
CC lipids, including oil, in tissues when the enzyme is absent or rate-
CC limiting, to isolate cDNAs and genes encoding homologous proteins from
CC the same or other plant species and to create transgenic plants in which
CC the polypeptides are present at higher or lower levels than normal or in
CC cell types or developmental stages in which they are not normally found,
CC thus altering the level of mono-, poly- and unsaturated fatty acids in
CC those cells. They are useful as probes for genetic and physical gene
CC mapping and as markers, e.g. restriction fragment length polymorphism
CC (RFLP) markers. The peptides can be used to immunise animals to produce
CC antibodies specific for the peptides and proteins. The present sequence
CC is plasmid pBS68 which is used for the suppression of diverged delta-9
CC desaturase in high stearate phenotypes. This sequence is used in the
CC exemplification of the invention. Note: The sequence data for this
CC sequence (AAD32909) corresponding to position 1501 to 6611 is not
CC represented in the printed specification but is based on the sequence
CC information supplied by the European patent office
XX
SQ Sequence 6611 BP; 1831 A; 1472 C; 1453 G; 1854 T; 0 U; 1 Other;
XX
XX Query Match 53.8%; Score 82.8; DB 6; Length 6611;
Best Local Similarity 97.7%; Pred. No. 5.4e-11;
Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 CGGCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCGCGGAGAGTGTGTCATCTCGCT 60
Db 5348 CGGCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCGCGGAGAGTGTGTCATCTCGCT 5407
QY 61 CATCGTCGAGTCGGCGCGGCGCGGACT 86
Db 5408 CATCGTCGAGTCGGCGCGGCGGCTGACT 5433
XX
RESULT 16
AAD32909/c
ID AAD32909 standard; DNA; 6611 BP.
XX
AC AAD32909;
XX
DT 01-JUL-2002 (first entry)
XX
DE pBS68 plasmid used for diverged delta-9 desaturase suppression.

XX Rice; diverged delta-9 fatty acid desaturase; enzyme; cellular lipid;
KW oil; transgenic plant; gene mapping; immunisation; plasmid pBS68; ds.
XX Unidentified.
XX
XX Key Location/Qualifiers
FH terminator 523. .725
FT /*tag= b
FT /label= Kit3_terminator
FT complement(880. .1920)
FT misc_feature /tag= b
FT /note= "Hygromycin selection region"
FT promoter 3260. .5348
FT /*tag= C
FT /label= Kit3_promoter
XX WO200216565-A2.
XX 28-FEB-2002.
XX
XX 22-AUG-2001; 2001WO-US026246.
XX
XX 22-AUG-2000; 2000US-0226996P.
XX
XX (DUPO) DU PONT DE NEMOURS & CO E I.
XX Booth JR, Cahoon RE, Hitz WD, Kinney AJ, Yadav NS;
XX WPI; 2002-269353/31.
XX
XX New delta-9 fatty acid desaturase polypeptides and polynucleotides,
PT useful in creating transgenic plants having altered levels of mono-, poly
PT - and unsaturated fatty acids and in increasing the unsaturation levels
PT in cellular lipids.
XX
XX Example 9; Page 76-77; 77pp; English.
XX
XX The present invention relates to diverged delta-9 fatty acid desaturase
CC proteins and polynucleotides encoding such proteins. The nucleic acid
CC sequences may be used to increase the level of unsaturation in cellular
CC lipids, including oil, in tissues when the enzyme is absent or rate-
CC limiting, to isolate cDNAs and genes encoding homologous proteins from
CC the same or other plant species and to create transgenic plants in which
CC the polypeptides are present at higher or lower levels than normal or in
CC cell types or developmental stages in which they are not normally found,
CC thus altering the level of mono-, poly- and unsaturated fatty acids in
CC those cells. They are useful as probes for genetic and physical gene
CC mapping and as markers, e.g. restriction fragment length polymorphism
CC (RFLP) markers. The peptides can be used to immunise animals to produce
CC antibodies specific for the peptides and proteins. The present sequence
CC is plasmid pBS68 which is used for the suppression of diverged delta-9
CC desaturase in high stearate phenotypes. This sequence is used in the
CC exemplification of the invention. Note: The sequence data for this
CC sequence (AAD32909) corresponding to position 1501 to 6611 is not
CC represented in the printed specification but is based on the sequence
CC information supplied by the European patent office
XX
SQ Sequence 6611 BP; 1831 A; 1472 C; 1453 G; 1854 T; 0 U; 1 Other;
XX
XX Query Match 53.8%; Score 82.8; DB 6; Length 6611;
Best Local Similarity 97.7%; Pred. No. 5.4e-11;
Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 69 AGTCGGCGCGCGCGGACTCGACGATGAGCGAGATGACCAAGCTCCGGCGCGGACTCGACG 128
Db 5433 ACTCAGCGCGCGCGGCGGACTCGACGATGAGCGAGATGACCAAGCTCCGGCGCGGACTCGACG 5374
QY 129 ATGAGCGGATGACCAAGCTCCGGCGG 154
Db 5373 ATGAGCGGATGACCAAGCTCCGGCGG 5348

RESULT 17
ABK10711
ID ABK10711 standard; DNA; 81 BP.
XX AC ABK10711;
XX DT 05-JUN-2002 (first entry)
XX DE Artificial DNA sequence #3.
XX KM Plastidic phosphoglucomutase; transgenic; plant; gene; ds.
XX OS Synthetic.
XX FH Key Location/Qualifiers
FT CDS 7..36
FT /*tag= a
FT /product= "ELVISLIVES peptide"
FT /partial
FT /note= "No start or stop codon shown"
FT 44..73
FT /*tag= b
FT /product= "ELVISLIVES peptide"
FT /partial
FT /note= "No start or stop codon shown"
XX PN EP1174510-A2.
XX PD 23-JAN-2002.
XX PF 17-JUL-2001; 2001EP-00306143.
XX PR 17-JUL-2000; 2000US-0218712P.
XX PA (DUPO) DU PONT DE NEMOURS & CO E I.
XX PI Allen SM, Butler KH, Carlson TJ, Ilag LL;
XX DR WPI; 2002-156692/21.
XX DR P-PSDB; AAU77109.
XX PT Novel isolated polypeptides having phosphoglucomutase activity and
PT polynucleotides encoding the polypeptides, useful for producing
PT transgenic plants with altered plastidic phosphoglucomutase protein
PT levels.
XX PS Example 9; Page 19; 27pp; English.
XX CC The invention relates to plastidic phosphoglucomutase polypeptides and
CC their related nucleic acids. The sequences are useful for producing a
CC transgenic plant, by transforming a plant cell with a polynucleotide of
CC the invention and regenerating a plant from the transformed plant cell.
CC Polynucleotide fragments are useful for suppressing the level of
CC expression of a gene encoding a polypeptide having plastidic
CC phosphoglucomutase activity. An isolated polynucleotide that affects the
CC level of expression of a plastidic phosphoglucomutase polypeptide in a
CC plant cell can be identified by introducing a DNA fragment comprising at
CC least 541 nucleotides, measuring the level of the polypeptide in the
CC plant cell containing the polynucleotide, and comparing the level of the
CC polypeptide in the plant cell containing the isolated polynucleotide with
CC the level of the polypeptide in a plant cell that does not contain the
CC isolated polynucleotide. A method for altering the level of expression of
CC a plastidic phosphoglucomutase protein in a host cell comprises
CC transforming a host cell with a chimeric gene and growing the transformed
CC cell under conditions that are suitable for expression of the chimeric
CC gene, where the expression of the gene results in production of altered
CC levels of plastidic phosphoglucomutase. This sequence represents an
CC artificial DNA used for plasmid construction, in the methods of the
CC invention
XX SQ Sequence 81 BP; 8 A; 28 C; 29 G; 16 T; 0 U; 0 Other;
Query Match 52.6%; Score 81; DB 6; Length 81;

Best Local Similarity 100.0%; Pred. No. 1.3e-10;
Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGGCCGAGCTGTGTCATCTCCTCATGTCGAGTCGGCGCCGAGAGCTGTGTCATCTCGCT 60
DB 1 CGGCCGAGCTGTGTCATCTCCTCATGTCGAGTCGGCGCCGAGAGCTGTGTCATCTCGCT 60
QY 61 CATCGTCGAGTCGGCGCCGCGC 81
DB 61 CATCGTCGAGTCGGCGCCGCGC 81
RESULT 18
ABK10711/c
ID ABK10711 standard; DNA; 81 BP.
XX AC ABK10711;
XX DT 05-JUN-2002 (first entry)
XX DE Artificial DNA sequence #3.
XX KM Plastidic phosphoglucomutase; transgenic; plant; gene; ds.
XX OS Synthetic.
XX FH Key Location/Qualifiers
FT CDS 7..36
FT /*tag= a
FT /product= "ELVISLIVES peptide"
FT /partial
FT /note= "No start or stop codon shown"
FT 44..73
FT /*tag= b
FT /product= "ELVISLIVES peptide"
FT /partial
FT /note= "No start or stop codon shown"
XX PN EP1174510-A2.
XX PD 23-JAN-2002.
XX PF 17-JUL-2001; 2001EP-00306143.
XX PR 17-JUL-2000; 2000US-0218712P.
XX PA (DUPO) DU PONT DE NEMOURS & CO E I.
XX PI Allen SM, Butler KH, Carlson TJ, Ilag LL;
XX DR WPI; 2002-156692/21.
XX DR P-PSDB; AAU77109.
XX PT Novel isolated polypeptides having phosphoglucomutase activity and
PT polynucleotides encoding the polypeptides, useful for producing
PT transgenic plants with altered plastidic phosphoglucomutase protein
PT levels.
XX PS Example 9; Page 19; 27pp; English.
XX CC The invention relates to plastidic phosphoglucomutase polypeptides and
CC their related nucleic acids. The sequences are useful for producing a
CC transgenic plant, by transforming a plant cell with a polynucleotide of
CC the invention and regenerating a plant from the transformed plant cell.
CC Polynucleotide fragments are useful for suppressing the level of
CC expression of a gene encoding a polypeptide having plastidic
CC phosphoglucomutase activity. An isolated polynucleotide that affects the
CC level of expression of a plastidic phosphoglucomutase polypeptide in a
CC plant cell can be identified by introducing a DNA fragment comprising at
CC least 541 nucleotides, measuring the level of the polypeptide in the
CC plant cell containing the polynucleotide, and comparing the level of the
CC polypeptide in the plant cell containing the isolated polynucleotide with
CC the level of the polypeptide in a plant cell that does not contain the

CC isolated polynucleotide. A method for altering the level of expression of
 CC a plastidic phosphoglucumutase protein in a host cell comprises
 CC transforming a host cell with a chimeric gene and growing the transformed
 CC cell under conditions that are suitable for expression of the chimeric
 CC gene, where the expression of the gene results in production of altered
 CC levels of plastidic phosphoglucumutase. This sequence represents an
 CC artificial DNA used for plasmid construction, in the methods of the
 CC invention

XX SQ Sequence 81 BP; 8 A; 28 C; 29 G; 16 T; 0 U; 0 Other;

XX Query Match 52.6%; Score 81; DB 6; Length 81;
 XX Best Local Similarity 100.0%; Pred. No. 1.3e-10;
 XX Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 74 GCGGCCCGCGACTCGACGATGAGCGAGTACCGAGCTCCGCCCGCGACTCGACGATGAG 133
 DB 81 GCGGCCCGCGACTCGACGATGAGCGAGTACCGAGCTCCGCCCGCGACTCGACGATGAG 22

OY 134 CGAGATGACCAAGCTCCGCCCG 154
 DB 21 CGAGATGACCAAGCTCCGCCCG 1

RESULT 19
 AAD29247
 ID AAD29247 standard; DNA; 963 BP.
 XX AAD29247;
 AC AAD29247;
 XX 07-MAY-2002 (first entry)
 DT 07-MAY-2002 (first entry)
 XX Plasmid pBS149 2X ELVISLIVES complementary region DNA.
 DE Plasmid pBS149 2X ELVISLIVES complementary region DNA.
 XX Recombinant construct; gene expression; late-soybean-embryo promoter;
 KM LEA; galactinol synthase; GAS1; GAS2; plasmid pBS149; ds.
 KW Unidentified.
 XX OS Unidentified.
 XX WO200200904-A2.
 PN WO200200904-A2.
 XX 03-JAN-2002.
 PD 03-JAN-2002.
 XX 22-JUN-2001; 2001WO-US019962.
 PF 22-JUN-2001; 2001WO-US019962.
 XX 23-JUN-2000; 2000US-0213961P.
 PR 23-JUN-2000; 2000US-0213961P.
 XX (DUPO) DU PONT DE NEMOURS & CO E I.
 PA (PION-) PIONEER HI-BRED INT INC.
 XX Glassman KF, Gordon-Kamm WJ, Kinney AJ, Lowe K, Stecca KL;
 PI Nichols SE;
 XX WPI; 2002-139927/18.
 DR WPI; 2002-139927/18.
 XX New recombinant construct having a promoter operably linked to a DNA
 PT sequence which when expressed produces an RNA having homology to a target
 PT mRNA and its reverse complement unrelated to endogenous DNA, for reducing
 PT gene expression.
 XX Example 10; Page 72; 77pp; English.

CC it. The present sequence is 2X ELVISLIVES complementary region from
 CC pBS149 that contains fragments from two soybean galactinol synthase genes
 CC GAS1 and GAS2. The region is functionally attached to a late-soybean-
 CC embryo promoter (LEA) and a phaseolin 3' terminator region. This entire
 CC region is then cloned into BamHI site of pK5136, which contains a 2X
 CC ELVISLIVES complementary region controlled by a soybean Kti promoter and
 CC terminator region used in the exemplification of the invention

XX SQ Sequence 963 BP; 240 A; 243 C; 248 G; 232 T; 0 U; 0 Other;

XX Query Match 52.6%; Score 81; DB 6; Length 963;
 XX Best Local Similarity 100.0%; Pred. No. 1.4e-10;
 XX Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 74 GCGGCCCGCGACTCGACGATGAGCGAGTACCGAGCTCCGCCCGCGACTCGACGATGAG 133
 DB 883 GCGGCCCGCGACTCGACGATGAGCGAGTACCGAGCTCCGCCCGCGACTCGACGATGAG 942

OY 134 CGAGATGACCAAGCTCCGCCCG 154
 DB 943 CGAGATGACCAAGCTCCGCCCG 963

RESULT 20
 AAD29247/c
 ID AAD29247 standard; DNA; 963 BP.
 XX AAD29247/c
 AC AAD29247;
 XX 07-MAY-2002 (first entry)
 DT 07-MAY-2002 (first entry)
 XX Plasmid pBS149 2X ELVISLIVES complementary region DNA.
 DE Plasmid pBS149 2X ELVISLIVES complementary region DNA.
 XX Recombinant construct; gene expression; late-soybean-embryo promoter;
 KM LEA; galactinol synthase; GAS1; GAS2; plasmid pBS149; ds.
 KW Unidentified.
 XX OS Unidentified.
 XX WO200200904-A2.
 PN WO200200904-A2.
 XX 03-JAN-2002.
 PD 03-JAN-2002.
 XX 22-JUN-2001; 2001WO-US019962.
 PF 22-JUN-2001; 2001WO-US019962.
 XX 23-JUN-2000; 2000US-0213961P.
 PR 23-JUN-2000; 2000US-0213961P.
 XX (DUPO) DU PONT DE NEMOURS & CO E I.
 PA (PION-) PIONEER HI-BRED INT INC.
 XX Glassman KF, Gordon-Kamm WJ, Kinney AJ, Lowe K, Stecca KL;
 PI Nichols SE;
 XX WPI; 2002-139927/18.
 DR WPI; 2002-139927/18.
 XX New recombinant construct having a promoter operably linked to a DNA
 PT sequence which when expressed produces an RNA having homology to a target
 PT mRNA and its reverse complement unrelated to endogenous DNA, for reducing
 PT gene expression.
 XX Example 10; Page 72; 77pp; English.

CC PBS149 that contains fragments from two soybean galactinol synthase genes
CC GAS1 and GAS2. The region is functionally attached to a late-soybean-
CC embryo promoter (UEA) and a phascolin 3' terminator region. This entire
CC region is then cloned into BamHI site of pKS136, which contains a 2X
CC ELVISLIVES complementary region controlled by a soybean Kti promoter and
CC terminator region used in the exemplification of the invention

XX SQ Sequence 963 BP; 240 A; 243 C; 248 G; 232 T; 0 U; 0 Other;

Query Match 52.6%; Score 81; DB 6; Length 963;
Best Local Similarity 100.0%; Pred. No. 1.4e-10;
Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CGGCCGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCGCGGAGCTGTCATCTCGCT 60
Db 963 CGGCCGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCGCGGAGCTGTCATCTCGCT 904

OY 61 CATCGTCGAGTCGGCGCGCGC 81
Db 903 CATCGTCGAGTCGGCGCGCGC 883

RESULT 21

AAD29230
ID AAD29230 standard; DNA; 80 BP.

XX AC AAD29230;

DT 07-MAY-2002 (first entry)

DE Plasmids pKS106, pKS124 1X ELVISLIVES complementary repeat DNA.

KW Recombinant construct; gene expression; plasmid pKS124; plasmid pKS106;
ds.

OS Unidentified.

Key Location/Qualifiers
FT CDS 7..36
FT CDS /*tag= a
FT CDS /product= "ELVISLIVES protein"
FT CDS complement(45..74)
FT CDS /*tag= b
FT CDS /product= "ELVISLIVES protein"

PN WO200200904-A2.

PD 03-JAN-2002.

PF 22-JUN-2001; 2001WO-US019962.

PR 23-JUN-2000; 2000US-0213961P.

PA (DUPO) DU PONT DE NEMOURS & CO E I.
PA (PION-) PIONEER HI-BRED INT INC.

PI Glassman KF, Gordon-Kamm WJ, Kinney AJ, Lowe K, Stecca KL;
PI Nichols SE;

DR WPI; 2002-139927/18.
DR P-PSDB; AAE18333.

PT New recombinant construct having a promoter operably linked to a DNA
PT sequence which when expressed produces an RNA having homology to a target
PT mRNA and its reverse complement unrelated to endogenous DNA, for reducing
PT gene expression.

PS Claim 45; Page 37; 77pp; English.

CC The present invention relates to a new recombinant construct. The
CC construct comprises a promoter operably linked to a DNA sequence which
CC when expressed by a host produces an RNA having homology to at least one
CC target mRNA expressed by the host and complementary RNA regions. The

CC recombinant construct is useful for reducing the expression of a target
CC mRNA or any similar endogenous mRNA. The RNAs expressed from the
CC recombinant constructs are also used in reducing expression of a target
CC mRNA or any similar endogenous mRNA. The sequences and their reverse
CC complements can be used to reduce the expression of any endogenous
CC genomic sequence that shares substantial similarity to nucleic acid
CC fragment which is in proximity to the DNA or RNA sequence derived from
CC it. The present sequence is 1X ELVISLIVES complementary repeat region DNA
CC found in plasmids pKS106 and pKS124 used in the exemplification of the
CC invention

XX SQ Sequence 80 BP; 12 A; 28 C; 28 G; 12 T; 0 U; 0 Other;

Query Match 51.9%; Score 80; DB 6; Length 80;
Best Local Similarity 100.0%; Pred. No. 2.2e-10;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 38 CGGCCGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCGCGCGGAGCTGTCATGAGC 97
Db 1 CGGCCGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCGCGCGGAGCTGTCATGAGC 60

OY 98 GAGATGACCACTCCGGCCG 117
Db 61 GAGATGACCACTCCGGCCG 80

RESULT 22

AAD29230/c
ID AAD29230 standard; DNA; 80 BP.

XX AC AAD29230;

DT 07-MAY-2002 (first entry)

DE Plasmids pKS106, pKS124 1X ELVISLIVES complementary repeat DNA.

KW Recombinant construct; gene expression; plasmid pKS124; plasmid pKS106;
ds.

OS Unidentified.

Key Location/Qualifiers
FT CDS 7..36
FT CDS /*tag= a
FT CDS /product= "ELVISLIVES protein"
FT CDS complement(45..74)
FT CDS /*tag= b
FT CDS /product= "ELVISLIVES protein"

PN WO200200904-A2.

PD 03-JAN-2002.

PF 22-JUN-2001; 2001WO-US019962.

PR 23-JUN-2000; 2000US-0213961P.

PA (DUPO) DU PONT DE NEMOURS & CO E I.
PA (PION-) PIONEER HI-BRED INT INC.

PI Glassman KF, Gordon-Kamm WJ, Kinney AJ, Lowe K, Stecca KL;
PI Nichols SE;

DR WPI; 2002-139927/18.
DR P-PSDB; AAE18333.

PT New recombinant construct having a promoter operably linked to a DNA
PT sequence which when expressed produces an RNA having homology to a target
PT mRNA and its reverse complement unrelated to endogenous DNA, for reducing
PT gene expression.

PS Claim 45; Page 37; 77pp; English.

CC The present invention relates to a new recombinant construct. The
CC construct comprises a promoter operably linked to a DNA sequence which
CC when expressed by a host produces an RNA having homology to at least one
CC target mRNA expressed by the host and complementary RNA regions. The

CC The present invention relates to a new recombinant construct. The
 CC construct comprises a promoter operably linked to a DNA sequence which
 CC when expressed by a host produces an RNA having homology to at least one
 CC target mRNA expressed by the host and complementary RNA regions. The
 CC recombinant construct is useful for reducing the expression of a target
 CC mRNA or any similar endogenous mRNA. The RNAs expressed from the
 CC recombinant constructs are also used in reducing expression of a target
 CC mRNA or any similar endogenous mRNA. The sequences and their reverse
 CC complements can be used to reduce the expression of any endogenous
 CC genomic sequence that shares substantial similarity to nucleic acid
 CC fragment which is in proximity to the DNA or RNA sequence derived from
 CC it. The present sequence is 1x ELVISLIVES complementary repeat region DNA
 CC found in plasmids pKS106 and pKS124 used in the exemplification of the
 CC invention
 XX
 SQ Sequence 80 BP; 12 A; 28 C; 28 G; 12 T; 0 U; 0 Other;
 Query Match 51.9%; Score 80; DB 6; Length 80;
 Best Local Similarity 100.0%; Pred. No. 2.2e-10;
 Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 38 CGGCCGAGCTGTCATCTCGCTCATCGTGCAGTCGGCGCCGCCGACTCGACGATGAGC 97
 DB 80 CGGCCGAGCTGTCATCTCGCTCATCGTGCAGTCGGCGCCGCCGACTCGACGATGAGC 21
 QY 98 GAGATGACCACTCCGGCCG 117
 DB 20 GAGATGACCACTCCGGCCG 1
 RESULT 23
 AAD32907
 ID AAD32907 standard; DNA; 80 BP.
 XX
 AC AAD32907;
 DT 01-JUL-2002 (first entry)
 XX
 DE Plasmids pKS106, pKS124 1x ELVISLIVES complementary repeat DNA.
 XX
 KM Diverged delta-9 fatty acid desaturase; enzyme; cellular lipid; oil;
 KM transgenic plant; gene mapping; immunisation; plasmid pKS124;
 KM plasmid pKS106; gene; ds.
 XX
 OS Unidentified.
 XX
 FH Key Location/Qualifiers
 FT CDS 7..36
 FT /*tag= a
 FT /product= "ELVISLIVES protein"
 FT CDS complement(45..74)
 FT /*tag= b
 FT /product= "ELVISLIVES protein"
 FT
 FT
 FT
 PN WO200216565-A2.
 XX
 PD 28-FEB-2002.
 XX
 PF 22-AUG-2001; 2001WO-US026246.
 XX
 PR 22-AUG-2000; 2000US-0226996P.
 XX
 PA (DUPO) DU PONT DE NEMOURS & CO E I.
 XX
 PI Booth JR, Cahoon RE, Hiltz WD, Kinney AJ, Yadav NS;
 XX
 DR WPI; 2002-269353/31.
 DR P-PSDB; AAE20554.
 XX
 PT New delta-9 fatty acid desaturase polypeptides and polynucleotides,
 PT useful in creating transgenic plants having altered levels of mono-, poly
 PT - and unsaturated fatty acids and in increasing the unsaturation levels
 PT in cellular lipids.

XX
 PS Example 9; Page 43; 77pp; English.
 XX
 CC The present invention relates to diverged delta-9 fatty acid desaturase
 CC proteins and polynucleotides encoding such proteins. The nucleic acid
 CC sequences may be used to increase the level of unsaturation in cellular
 CC lipids, including oil, in tissues when the enzyme is absent or rate-
 CC limiting, to isolate cDNAs and genes encoding homologous proteins from
 CC the same or other plant species and to create transgenic plants in which
 CC the polypeptides are present at higher or lower levels than normal or in
 CC cell types or developmental stages in which they are not normally found,
 CC thus altering the level of mono-, poly- and unsaturated fatty acids in
 CC those cells. They are useful as probes for genetic and physical gene
 CC mapping and as markers, e.g. restriction fragment length polymorphism
 CC (RFLP) markers. The peptides can be used to immunise animals to produce
 CC antibodies specific for the peptides and proteins. The present sequence
 CC is 1x ELVISLIVES complementary repeat region DNA found in plasmids pKS106
 CC and pKS124. This sequence is used in the exemplification of the invention
 CC for the suppression of Fad2 in soybean
 XX
 SQ Sequence 80 BP; 12 A; 28 C; 28 G; 12 T; 0 U; 0 Other;
 Query Match 51.9%; Score 80; DB 6; Length 80;
 Best Local Similarity 100.0%; Pred. No. 2.2e-10;
 Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 38 CGGCCGAGCTGTCATCTCGCTCATCGTGCAGTCGGCGCCGCCGACTCGACGATGAGC 97
 DB 1 CGGCCGAGCTGTCATCTCGCTCATCGTGCAGTCGGCGCCGCCGACTCGACGATGAGC 60
 QY 98 GAGATGACCACTCCGGCCG 117
 DB 61 GAGATGACCACTCCGGCCG 80
 RESULT 24
 AAD32907/c
 ID AAD32907 standard; DNA; 80 BP.
 XX
 AC AAD32907;
 DT 01-JUL-2002 (first entry)
 XX
 DE Plasmids pKS106, pKS124 1x ELVISLIVES complementary repeat DNA.
 XX
 KM Diverged delta-9 fatty acid desaturase; enzyme; cellular lipid; oil;
 KM transgenic plant; gene mapping; immunisation; plasmid pKS124;
 KM plasmid pKS106; gene; ds.
 XX
 OS Unidentified.
 XX
 FH Key Location/Qualifiers
 FT CDS 7..36
 FT /*tag= a
 FT /product= "ELVISLIVES protein"
 FT CDS complement(45..74)
 FT /*tag= b
 FT /product= "ELVISLIVES protein"
 FT
 FT
 FT
 PN WO200216565-A2.
 XX
 PD 28-FEB-2002.
 XX
 PF 22-AUG-2001; 2001WO-US026246.
 XX
 PR 22-AUG-2000; 2000US-0226996P.
 XX
 PA (DUPO) DU PONT DE NEMOURS & CO E I.
 XX
 PI Booth JR, Cahoon RE, Hiltz WD, Kinney AJ, Yadav NS;
 XX
 DR WPI; 2002-269353/31.
 DR P-PSDB; AAE20554.

XX New delta-9 fatty acid desaturase polypeptides and polynucleotides,
PT useful in creating transgenic plants having altered levels of mono-, poly
PT - and unsaturated fatty acids and in increasing the unsaturation levels
PT in cellular lipids.
XX
PS Example 9; Page 43; 77pp; English.
XX
CC The present invention relates to diverged delta-9 fatty acid desaturase
CC proteins and polynucleotides encoding such proteins. The nucleic acid
CC sequences may be used to increase the level of unsaturation in cellular
CC lipids, including oil, in tissues when the enzyme is absent or rate-
CC limiting, to isolate cDNAs and genes encoding homologous proteins from
CC the same or other plant species and to create transgenic plants in which
CC the polypeptides are present at higher or lower levels than normal or in
CC cell types or developmental stages in which they are not normally found,
CC thus altering the level of mono-, poly- and unsaturated fatty acids in
CC those cells. They are useful as probes for genetic and physical gene
CC mapping and as markers, e.g. restriction fragment length polymorphism
CC (RFLP) markers. The peptides can be used to immunise animals to produce
CC antibodies specific for the peptides and proteins. The present sequence
CC is 1X ELVISLIVES complementary repeat region DNA found in plasmids PKS106
CC and PKS124. This sequence is used in the exemplification of the invention
CC for the suppression of Fad2 in soybean
XX
SQ Sequence 80 BP; 12 A; 28 C; 28 G; 12 T; 0 U; 0 Other;

Query Match 51.9%; Score 80; DB 6; Length 80;
Best Local Similarity 100.0%; Pred. No. 2.2e-10;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 CGGCCGAGCTGTGTCATCTCGCTCATGTCGAGTCGGCGCGCCGACTCGACGATGAGC 97
Db 80 CGGCCGAGCTGTGTCATCTCGCTCATGTCGAGTCGGCGCGCCGACTCGACGATGAGC 21
QY 98 GAGATGACCAAGCTCCGGCCG 117
Db 20 GAGATGACCAAGCTCCGGCCG 1

RESULT 25
ABK10712
ID ABK10712 standard; DNA; 92 BP.
XX
AC ABK10712;
XX
DT 05-JUN-2002 (first entry)
XX
DE Artificial DNA sequence #4.
XX
KM Plastidic phosphoglucumutase; transgenic; plant; gene; ss.
XX
OS Synthetic.
XX
PN EP1174510-A2.
XX
PD 23-JAN-2002.
XX
PF 17-JUL-2001; 2001EP-00306143.
XX
PR 17-JUL-2000; 2000US-0218712P.
XX
PA (DUPO) DU PONT DE NEMOURS & CO E I.
XX
PI Allen SM, Butler KH, Carlson TJ, Ilag LL;
XX
DR WPI; 2002-156692/21.
XX
PT Novel isolated polypeptides having phosphoglucumutase activity and
PT polynucleotides encoding the polypeptides, useful for producing
PT transgenic plants with altered plastidic phosphoglucumutase protein
PT levels.
XX

PS Example 9; Page 19; 27pp; English.
XX
CC The invention relates to plastidic phosphoglucumutase polypeptides and
CC their related nucleic acids. The sequences are useful for producing a
CC transgenic plant, by transforming a plant cell with a polynucleotide of
CC the invention and regenerating a plant from the transformed plant cell.
CC Polynucleotide fragments are useful for suppressing the level of
CC expression of a gene encoding a polypeptide having plastidic
CC phosphoglucumutase activity. An isolated polynucleotide that affects the
CC level of expression of a plastidic phosphoglucumutase polypeptide in a
CC plant cell can be identified by introducing a DNA fragment comprising at
CC least 541 nucleotides, measuring the level of the polypeptide in the
CC plant cell containing the polynucleotide, and comparing the level of the
CC polypeptide in the plant cell containing the isolated polynucleotide with
CC the level of the polypeptide in a plant cell that does not contain the
CC isolated polynucleotide. A method for altering the level of expression of
CC a plastidic phosphoglucumutase protein in a host cell comprises
CC transforming a host cell with a chimeric gene and growing the transformed
CC cell under conditions that are suitable for expression of the chimeric
CC gene, where the expression of the gene results in production of altered
CC levels of plastidic phosphoglucumutase. This sequence represents an
CC artificial DNA used for plasmid construction, in the methods of the
CC invention
XX
SQ Sequence 92 BP; 16 A; 30 C; 30 G; 16 T; 0 U; 0 Other;

Query Match 51.9%; Score 80; DB 6; Length 92;
Best Local Similarity 100.0%; Pred. No. 2.2e-10;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 CGGCCGAGCTGTGTCATCTCGCTCATGTCGAGTCGGCGCGCCGACTCGACGATGAGC 97
Db 7 CGGCCGAGCTGTGTCATCTCGCTCATGTCGAGTCGGCGCGCCGACTCGACGATGAGC 66
QY 98 GAGATGACCAAGCTCCGGCCG 117
Db 67 GAGATGACCAAGCTCCGGCCG 86

RESULT 26
ABK10712/c
ID ABK10712 standard; DNA; 92 BP.
XX
AC ABK10712;
XX
DT 05-JUN-2002 (first entry)
XX
DE Artificial DNA sequence #4.
XX
KM Plastidic phosphoglucumutase; transgenic; plant; gene; ss.
XX
OS Synthetic.
XX
PN EP1174510-A2.
XX
PD 23-JAN-2002.
XX
PF 17-JUL-2001; 2001EP-00306143.
XX
PR 17-JUL-2000; 2000US-0218712P.
XX
PA (DUPO) DU PONT DE NEMOURS & CO E I.
XX
PI Allen SM, Butler KH, Carlson TJ, Ilag LL;
XX
DR WPI; 2002-156692/21.
XX
PT Novel isolated polypeptides having phosphoglucumutase activity and
PT polynucleotides encoding the polypeptides, useful for producing
PT transgenic plants with altered plastidic phosphoglucumutase protein
PT levels.
XX
XX Example 9; Page 19; 27pp; English.

XX The invention relates to plastidic phosphoglucomutase polypeptides and
CC their related nucleic acids. The sequences are useful for producing a
CC transgenic plant, by transforming a plant cell with a polynucleotide of
CC the invention and regenerating a plant from the transformed plant cell.
CC Polynucleotide fragments are useful for suppressing the level of
CC expression of a gene encoding a polypeptide having plastidic
CC phosphoglucomutase activity. An isolated polynucleotide that affects the
CC level of expression of a plastidic phosphoglucomutase polypeptide in a
CC plant cell can be identified by introducing a DNA fragment comprising at
CC least 541 nucleotides, measuring the level of the polypeptide in the
CC plant cell containing the polynucleotide, and comparing the level of the
CC polypeptide in the plant cell containing the isolated polynucleotide with
CC the level of the polypeptide in a plant cell that does not contain the
CC isolated polynucleotide. A method for altering the level of expression of
CC a plastidic phosphoglucomutase protein in a host cell comprises
CC transforming a host cell with a chimeric gene and growing the transformed
CC cell under conditions that are suitable for expression of the chimeric
CC gene, where the expression of the gene results in production of altered
CC levels of plastidic phosphoglucomutase. This sequence represents an
CC artificial DNA used for plasmid construction, in the methods of the
CC invention

XX Sequence 92 BP; 16 A; 30 C; 30 G; 16 T; 0 U; 0 Other;

Query Match 51.9%; Score 80; DB 6; Length 92;
Best Local Similarity 100.0%; Pred. No. 2.2e-10;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 38 CGGCCGAGCTGTGTCATCTCGCTCATCTCGAGTCGGCGCCGCCGACTCGACGATGAGC 97
DB 86 CGGCCGAGCTGTGTCATCTCGCTCATCTCGAGTCGGCGCCGCCGACTCGACGATGAGC 27

OY 98 GAGATGACCAGCTCCGGCCG 117
DB 26 GAGATGACCAGCTCCGGCCG 7

RESULT 27

AAD29232
ID AAD29232 standard; DNA; 92 BP.

XX AAD29232;

DT 07-MAY-2002 (first entry)

XX ELVISLIVES complementary region DNA amplifying PCR primer #1.

KW Recombinant construct; gene expression; PCR primer; ss.

XX Unidentified.

PN WO200200904-A2.

PD 03-JAN-2002.

PF 22-JUN-2001; 2001WO-US019962.

PR 23-JUN-2000; 2000US-0213961P.

PA (DUPO) DU PONT DE NEMOURS & CO E I.

PI (PION-) PIONEER HI-BRED INT INC.

PI Glassman KF, Gordon-Kamm WJ, Kinney AJ, Lowe K, Stecca KL;
PI Nichols SE;

DR WPI; 2002-139927/18.

PT New recombinant construct having a promoter operably linked to a DNA
PT sequence which when expressed produces an RNA having homology to a target
PT mRNA and its reverse complement unrelated to endogenous DNA, for reducing
PT gene expression.

PS Example 7; Page 37; 77pp; English.

XX The present invention relates to a new recombinant construct. The
CC construct comprises a promoter operably linked to a DNA sequence which
CC when expressed by a host produces an RNA having homology to at least one
CC target mRNA expressed by the host and complementary RNA regions. The
CC recombinant construct is useful for reducing the expression of a target
CC mRNA or any similar endogenous mRNA. The RNAs expressed from the
CC recombinant constructs are also used in reducing expression of a target
CC mRNA or any similar endogenous mRNA. The sequences and their reverse
CC complements can be used to reduce the expression of any endogenous
CC genomic sequence that shares substantial similarity to nucleic acid
CC fragment which is in proximity to the DNA or RNA sequence derived from
CC it. The present sequence is a PCR primer used for amplifying ELVISLIVES
CC complementary region DNA used in the exemplification of the invention

XX Sequence 92 BP; 16 A; 30 C; 30 G; 16 T; 0 U; 0 Other;

Query Match 51.9%; Score 80; DB 6; Length 92;
Best Local Similarity 100.0%; Pred. No. 2.2e-10;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 38 CGGCCGAGCTGTGTCATCTCGCTCATCTCGAGTCGGCGCCGCCGACTCGACGATGAGC 97
DB 7 CGGCCGAGCTGTGTCATCTCGCTCATCTCGAGTCGGCGCCGCCGACTCGACGATGAGC 66

OY 98 GAGATGACCAGCTCCGGCCG 117
DB 67 GAGATGACCAGCTCCGGCCG 86

RESULT 28

AAD29232/c
ID AAD29232 standard; DNA; 92 BP.

XX AAD29232;

DT 07-MAY-2002 (first entry)

XX ELVISLIVES complementary region DNA amplifying PCR primer #1.

KW Recombinant construct; gene expression; PCR primer; ss.

XX Unidentified.

PN WO200200904-A2.

PD 03-JAN-2002.

PF 22-JUN-2001; 2001WO-US019962.

PR 23-JUN-2000; 2000US-0213961P.

PA (DUPO) DU PONT DE NEMOURS & CO E I.

PI (PION-) PIONEER HI-BRED INT INC.

PI Glassman KF, Gordon-Kamm WJ, Kinney AJ, Lowe K, Stecca KL;
PI Nichols SE;

DR WPI; 2002-139927/18.

PT New recombinant construct having a promoter operably linked to a DNA
PT sequence which when expressed produces an RNA having homology to a target
PT mRNA and its reverse complement unrelated to endogenous DNA, for reducing
PT gene expression.

PS Example 7; Page 37; 77pp; English.

XX The present invention relates to a new recombinant construct. The
CC construct comprises a promoter operably linked to a DNA sequence which
CC when expressed by a host produces an RNA having homology to at least one
CC target mRNA expressed by the host and complementary RNA regions. The
CC recombinant construct is useful for reducing the expression of a target

CC mRNA or any similar endogenous mRNA. The RNAs expressed from the
CC recombinant constructs are also used in reducing expression of a target
CC mRNA or any similar endogenous mRNA. The sequences and their reverse
CC complements can be used to reduce the expression of any endogenous
CC genomic sequence that shares substantial similarity to nucleic acid
CC fragment which is in proximity to the DNA or RNA sequence derived from
CC it. The present sequence is a PCR primer used for amplifying ELVISLIVES
CC complementary region DNA used in the exemplification of the invention
XX
SQ Sequence 92 BP; 16 A; 30 C; 30 G; 16 T; 0 U; 0 Other;

Query Match 51.9%; Score 80; DB 6; Length 92;
Best Local Similarity 100.0%; Pred. No. 2.2e-10;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 38 CGCCCGAGCTGTCATCTCGCTCATCGAGTCGCGCGCCCGCGACTCGACGATGAGC 97
DB 86 CGCCCGAGCTGTCATCTCGCTCATCGAGTCGCGCGCCCGCGACTCGACGATGAGC 27
OY 98 GAGATGACCACTCCGCCG 117
DB 26 GAGATGACCACTCCGCCG 7

RESULT 29
AAD29242
ID AAD29242 standard; DNA; 1717 BP.
XX
AC AAD29242;
XX
DT 07-MAY-2002 (first entry)
XX
DE Plasmid pBS68 2X ELVISLIVES complementary region DNA.
XX
KW Recombinant construct; gene expression; soybean; fatty acid desaturase;
KM Fad2-1; delta-9 desaturase; plasmid pBS68; ds.
XX
OS Unidentified.
XX
PN WO200200904-A2.
XX
PD 03-JAN-2002.
XX
PF 22-JUN-2001; 2001WO-US019962.
XX
PR 23-JUN-2000; 2000US-0213961P.
XX
PA (DUPO) DU PONT DE NEMOURS & CO E I.
PA (PION-) PIONEER HI-BRED INT INC.
XX
PI Glassman KF, Gordon-Kamm WJ, Kinney AJ, Lowe K, Stecca KL;
PI Nichols SE;
XX
DR WPI; 2002-139927/18.
XX
PT New recombinant construct having a promoter operably linked to a DNA
PT sequence which when expressed produces an RNA having homology to a target
PT mRNA and its reverse complement unrelated to endogenous DNA, for reducing
PT gene expression.
XX
PS Example 9; Page 70; 77pp; English.
XX
CC The present invention relates to a new recombinant construct. The
CC construct comprises a promoter operably linked to a DNA sequence which
CC when expressed by a host produces an RNA having homology to at least one
CC target mRNA expressed by the host and complementary RNA regions. The
CC recombinant construct is useful for reducing the expression of a target
CC mRNA or any similar endogenous mRNA. The RNAs expressed from the
CC recombinant constructs are also used in reducing expression of a target
CC mRNA or any similar endogenous mRNA. The sequences and their reverse
CC complements can be used to reduce the expression of any endogenous
CC genomic sequence that shares substantial similarity to nucleic acid
CC fragment which is in proximity to the DNA or RNA sequence derived from

CC it. The present sequence is 2X ELVISLIVES complementary region from pBS68
CC which contains 2X ELVISLIVES complementary regions surrounding the the
CC nucleotide Fad2-1 NotI fragment from pKSI11 and a nucleotide fragment
CC from a soybean delta-9 desaturase gene used in the exemplification of the
CC invention
XX
SQ Sequence 1717 BP; 399 A; 430 C; 478 G; 410 T; 0 U; 0 Other;

Query Match 29.7%; Score 45.8; DB 6; Length 1717;
Best Local Similarity 95.9%; Pred. No. 0.048;
Matches 47; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 38 CGCCCGAGCTGTCATCTCGCTCATCGAGTCGCGCGCCCGCGACT 86
DB 1 CGCCCGAGCTGTCATCTCGCTCATCGAGTCGCGCGCCCGCTGAGT 49

RESULT 30
AAD29242/c
ID AAD29242 standard; DNA; 1717 BP.
XX
AC AAD29242;
XX
DT 07-MAY-2002 (first entry)
XX
DE Plasmid pBS68 2X ELVISLIVES complementary region DNA.
XX
KW Recombinant construct; gene expression; soybean; fatty acid desaturase;
KM Fad2-1; delta-9 desaturase; plasmid pBS68; ds.
XX
OS Unidentified.
XX
PN WO200200904-A2.
XX
PD 03-JAN-2002.
XX
PF 22-JUN-2001; 2001WO-US019962.
XX
PR 23-JUN-2000; 2000US-0213961P.
XX
PA (DUPO) DU PONT DE NEMOURS & CO E I.
PA (PION-) PIONEER HI-BRED INT INC.
XX
PI Glassman KF, Gordon-Kamm WJ, Kinney AJ, Lowe K, Stecca KL;
PI Nichols SE;
XX
DR WPI; 2002-139927/18.
XX
PT New recombinant construct having a promoter operably linked to a DNA
PT sequence which when expressed produces an RNA having homology to a target
PT mRNA and its reverse complement unrelated to endogenous DNA, for reducing
PT gene expression.
XX
PS Example 9; Page 70; 77pp; English.
XX
CC The present invention relates to a new recombinant construct. The
CC construct comprises a promoter operably linked to a DNA sequence which
CC when expressed by a host produces an RNA having homology to at least one
CC target mRNA expressed by the host and complementary RNA regions. The
CC recombinant construct is useful for reducing the expression of a target
CC mRNA or any similar endogenous mRNA. The RNAs expressed from the
CC recombinant constructs are also used in reducing expression of a target
CC mRNA or any similar endogenous mRNA. The sequences and their reverse
CC complements can be used to reduce the expression of any endogenous
CC genomic sequence that shares substantial similarity to nucleic acid
CC fragment which is in proximity to the DNA or RNA sequence derived from
CC it. The present sequence is 2X ELVISLIVES complementary region from pBS68
CC which contains 2X ELVISLIVES complementary regions surrounding the the
CC nucleotide Fad2-1 NotI fragment from pKSI11 and a nucleotide fragment
CC from a soybean delta-9 desaturase gene used in the exemplification of the
CC invention
XX
SQ Sequence 1717 BP; 399 A; 430 C; 478 G; 410 T; 0 U; 0 Other;

CC gene, where the expression of the gene results in production of altered
CC levels of plasmidic phosphoglucosyltransferase. This sequence represents an
CC artificial DNA used for plasmid construction, in the methods of the
CC invention
XX
SQ Sequence 44 BP; 4 A; 16 C; 16 G; 8 T; 0 U; 0 Other;
Query Match 28.6%; Score 44; DB 6; Length 44;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 74 GCGGCGCGGACTGACGATGAGCAGCTCCGCGG 117
DB 44 GCGGCGCGGACTGACGATGAGCAGCTCCGCGG 1
RESULT 33
ADS14722
ID ADS14722 standard; DNA; 1251 BP.
XX
AC ADS14722;
XX
DT 16-DEC-2004 (first entry)
XX
DE Pseudomonas aeruginosa quorum sensing controlled gene PA4304, SEQ ID 277.
XX
KW Cytostatic; Anti-HIV; Antimicrobial; Immunosuppressive;
KW quorum sensing signalling; bacterium; quorum sensing controlled gene;
KW biofilm-associated disease; cystic fibrosis; AIDS; middle ear infection;
KW acne; periodontal disease; gene; ds; PA4304.
XX
OS Pseudomonas aeruginosa.
XX
PN WO2004083385-A2.
XX
PD 30-SEP-2004.
XX
PF 11-MAR-2004; 2004WO-US007467.
XX
PR 14-MAR-2003; 2003US-00389647.
XX
PA (IOWA) UNIV IOWA RES FOUND.
XX
PI Greenberg BP, Schuster M, Lostroh C;
XX
DR WPI; 2004-709932/69.
XX
PT Identifying a modulator of quorum sensing signaling in bacteria, useful
PT for treating a biofilm-associated disorder, comprises contacting the cell
PT with a quorum sensing signal molecule in the presence and absence of a
PT test compound.
XX
PS Disclosure; SEQ ID NO 277; 233pp; English.
XX
CC The present invention relates to a method for identifying a modulator of
CC quorum sensing signalling in bacteria. The method comprises: providing a
CC cell that comprises a quorum sensing controlled gene (ADS14446-ADS14798),
CC where the cell is responsive to a quorum sensing signal molecule such
CC that a detectable signal is generated; contacting the cell with a quorum
CC sensing signal molecule in the presence and absence of a test compound;
CC and detecting a change in the detectable signal. The method and modulator
CC identified by the method are useful for treating a biofilm-associated
CC disease or disorder, e.g. cystic fibrosis, AIDS, middle ear infections,
CC acne, periodontal disease, catheter-associated infections, and medical
CC device-associated infections. Note: The sequence data for this patent was
CC obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1251 BP; 205 A; 412 C; 436 G; 198 T; 0 U; 0 Other;
Query Match 24.8%; Score 38.2; DB 13; Length 1251;
Best Local Similarity 61.6%; Pred. No. 3.3;
Matches 61; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

OY 37 GCGGCGGAGCTGTGTCATCTCGTCATCGAGTCGCGCGCGCGGCGGACTCGACATGAG 96
DB 1080 GCTGCTGATGATCGTCAACCCCGCACTGTGTCAGCCGCTGGCGCGGACGACAGTTGCC 1139
OY 97 CGAGATGACCACTCCGCGCGCGGACTCGACGATGAGCG 135
DB 1140 GGACCTGCGCGCGGAGGCGCTGCGGCACTACGATCCGGG 1178
RESULT 34
ADS14722/c
ID ADS14722 standard; DNA; 1251 BP.
XX
AC ADS14722;
XX
DT 16-DEC-2004 (first entry)
XX
DE Pseudomonas aeruginosa quorum sensing controlled gene PA4304, SEQ ID 277.
XX
KW Cytostatic; Anti-HIV; Antimicrobial; Immunosuppressive;
KW quorum sensing signalling; bacterium; quorum sensing controlled gene;
KW biofilm-associated disease; cystic fibrosis; AIDS; middle ear infection;
KW acne; periodontal disease; gene; ds; PA4304.
XX
OS Pseudomonas aeruginosa.
XX
PN WO2004083385-A2.
XX
PD 30-SEP-2004.
XX
PF 11-MAR-2004; 2004WO-US007467.
XX
PR 14-MAR-2003; 2003US-00389647.
XX
PA (IOWA) UNIV IOWA RES FOUND.
XX
PI Greenberg BP, Schuster M, Lostroh C;
XX
DR WPI; 2004-709932/69.
XX
PT Identifying a modulator of quorum sensing signaling in bacteria, useful
PT for treating a biofilm-associated disorder, comprises contacting the cell
PT with a quorum sensing signal molecule in the presence and absence of a
PT test compound.
XX
PS Disclosure; SEQ ID NO 277; 233pp; English.
XX
CC The present invention relates to a method for identifying a modulator of
CC quorum sensing signalling in bacteria. The method comprises: providing a
CC cell that comprises a quorum sensing controlled gene (ADS14446-ADS14798),
CC where the cell is responsive to a quorum sensing signal molecule such
CC that a detectable signal is generated; contacting the cell with a quorum
CC sensing signal molecule in the presence and absence of a test compound;
CC and detecting a change in the detectable signal. The method and modulator
CC identified by the method are useful for treating a biofilm-associated
CC disease or disorder, e.g. cystic fibrosis, AIDS, middle ear infections,
CC acne, periodontal disease, catheter-associated infections, and medical
CC device-associated infections. Note: The sequence data for this patent was
CC obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1251 BP; 205 A; 412 C; 436 G; 198 T; 0 U; 0 Other;
Query Match 24.8%; Score 38.2; DB 13; Length 1251;
Best Local Similarity 61.6%; Pred. No. 3.3;
Matches 61; Conservative 0; Mismatches 38; Indels 0; Gaps 0;
OY 20 CGTCATCTGTCAGTCGCGCGCGGAGCTGTGTCATCTCGTCATCTGTCAGTCGCGCGG 79
DB 1178 CCGGATCTGATGTCGCGGAGGCGCTCGCGGAGGTCGCGCACTGTGTCGCGCGG 1119
OY 80 GCGGACTCGACGATGAGCGAGATGACCACTCCGCGCGG 118

Db 1118 AGCGGCTGACCAAGTGTGGGTGACGATCATCAGCAGC 1080

RESULT 35
ADJ40055

ID ADJ40055 standard; cDNA; 2730 BP.

XX ADJ40055;

DT 06-MAY-2004 (first entry)

XX Plant cDNA #1055.

KW Plant; gene; ss; transcription; plant genome augmentation; cereal;
KW soybean; alfalfa; sunflower; canola; cotton; peanut; tobacco; sugar beet;
KW maize; barley; sorghum; rice; wheat; crop plant; insecticide resistance;
KW stress tolerance; salt tolerance; cold tolerance; drought tolerance;
KW plant nutrition; apical dominance; dwarfism; early flowering; antiviral;
antifungal.

XX Eukaryota.

PN US2004016025-A1.

PD 22-JAN-2004.

PF 26-SEP-2002; 2002US-00260238.

PR 26-SEP-2001; 2001US-0325277P.

PR 26-SEP-2001; 2001US-0325448P.

PR 04-APR-2002; 2002US-0370620P.

PA (BUDW/) BUDWORTH P.
PA (MOUG/) MOUGHAMER T.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZEBROOK J.
PA (GOFF/) GOFF S A.
PA (KATA/) KATAGIRI F.
PA (KREP/) KREPS J.
PA (PROV/) PROVART N.
PA (RICK/) RICHE D.
PA (ZHUT/) ZHU T.

PI Budworth P, Moughamer T, Briggs SP, Cooper B, Glazebrook J;
PI Goff SA, Katagiri F, Kreps J, Provart N, Riche D, Zhu T;

XX WPI; 2004-190374/18.

PT New rice promoter, useful for manipulating crop plants to alter or
PT improve phenotypic characteristics, e.g. produce large quantities of oil
PT or proteins, resistance to insecticides, virus or fungi, stress tolerance
PT or high nutritional value.

PS Claim 25; SEQ ID NO 1055; 230pp; English.

CC The invention relates to plant nucleotide sequences that direct seed-
CC leaf- and/or stem-, panicle-, root- or pollen-specific or -preferential
CC or constitutive transcription of an operatively linked nucleic acid
CC segment. The invention also relates to a method for augmenting a plant
CC genome and a method of identifying a gene, where its expression is
CC altered in the seed, leaf, stem, panicle, pollen, root or is constitutive
CC in a plant cell. The plant is a cereal, e.g. soybean, alfalfa, sunflower,
CC canola, cotton, peanut, tobacco or sugar beet, preferably maize, barley,
CC sorghum, rice or wheat. The polynucleotides and the polypeptides they
CC encode are useful for manipulating crop plants to alter or improve
CC phenotypic characteristics, to produce large quantities of oil or
CC proteins, to incur resistance to insecticides, viruses or fungi, and to
CC incur stress tolerance (e.g. salt, cold or drought) to ensure the plants
CC have a high nutritional value with reduced apical dominance or dwarfism,
CC early flowering or altered metabolic pathways. This sequence represents a
CC plant nucleic acid of the invention. Note: The sequence data for this

CC patent did not form part of the printed specification but was obtained in
CC electronic format directly from USPTO at seqdata.uspto.gov/sequence.html.
XX

SQ Sequence 2730 BP; 470 A; 1009 C; 847 G; 400 T; 0 U; 4 Other;

Query Match 22.9%; Score 35.2; DB 12; Length 2730;
Best Local Similarity 56.6%; Pred. No. 18;
Matches 64; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

OY 1 CGCCGAGCTGTCATCTGCTCATCTGTCGAGTCGGCGCGGAGCTGTCATCTGCT 60

DB 31 CGCAAGCGCTCCAGTCGCTGACACGAGGTTGCTGCTGCCGCGGTGCGCTGCGCT 90

OY 61 CATCTGAGTCGCGCGCGCGCGAGCTGACGATGAGCGAGATGACCACTCGG 113

DB 91 CGTCGTGCG 143

RESULT 36

ADJ40055/c

ID ADJ40055 standard; cDNA; 2730 BP.

XX ADJ40055;

DT 06-MAY-2004 (first entry)

DE Plant cDNA #1055.

KW Plant; gene; ss; transcription; plant genome augmentation; cereal;
KW soybean; alfalfa; sunflower; canola; cotton; peanut; tobacco; sugar beet;
KW maize; barley; sorghum; rice; wheat; crop plant; insecticide resistance;
KW stress tolerance; salt tolerance; cold tolerance; drought tolerance;
KW plant nutrition; apical dominance; dwarfism; early flowering; antiviral;
antifungal.

XX Eukaryota.

PN US2004016025-A1.

PD 22-JAN-2004.

PF 26-SEP-2002; 2002US-00260238.

PR 26-SEP-2001; 2001US-0325277P.

PR 26-SEP-2001; 2001US-0325448P.

PR 04-APR-2002; 2002US-0370620P.

PA (BUDW/) BUDWORTH P.
PA (MOUG/) MOUGHAMER T.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZEBROOK J.
PA (GOFF/) GOFF S A.
PA (KATA/) KATAGIRI F.
PA (KREP/) KREPS J.
PA (PROV/) PROVART N.
PA (RICK/) RICHE D.
PA (ZHUT/) ZHU T.

PI Budworth P, Moughamer T, Briggs SP, Cooper B, Glazebrook J;
PI Goff SA, Katagiri F, Kreps J, Provart N, Riche D, Zhu T;

XX WPI; 2004-190374/18.

PT New rice promoter, useful for manipulating crop plants to alter or
PT improve phenotypic characteristics, e.g. produce large quantities of oil
PT or proteins, resistance to insecticides, virus or fungi, stress tolerance
PT or high nutritional value.

PS Claim 25; SEQ ID NO 1055; 230pp; English.

CC The invention relates to plant nucleotide sequences that direct seed-
CC leaf- and/or stem-, panicle-, root- or pollen-specific or -preferential

CC or constitutive transcription of an operatively linked nucleic acid
CC segment. The invention also relates to a method for augmenting a plant
CC genome and a method of identifying a gene, where its expression is
CC altered in the seed, leaf, stem, panicle, pollen, root or is constitutive
CC in a plant cell. The plant is a cereal, e.g. soybean, alfalfa, sunflower,
CC canola, cotton, peanut, tobacco or sugar beet, preferably maize, barley,
CC sorghum, rice or wheat. The polynucleotides and the polypeptides they
CC encode are useful for manipulating crop plants to alter or improve
CC phenotypic characteristics, to produce large quantities of oil or
CC proteins, to incur resistance to insecticides, viruses or fungi, and to
CC incur stress tolerance (e.g. salt, cold or drought) to ensure the plants
CC have a high nutritional value with reduced apical dominance or dwarfism,
CC early flowering or altered metabolic pathways. This sequence represents a
CC plant nucleic acid of the invention. Note: The sequence data for this
CC patent did not form part of the printed specification but was obtained in
CC electronic format directly from USPTO at seqdata.uspto.gov/sequence.html.
XX
SQ Sequence 2730 BP; 470 A; 1009 C; 847 G; 400 T; 0 U; 4 Other;

Query Match 22.9%; Score 35.2; DB 12; Length 2730;
Best Local Similarity 56.6%; Pred. No. 18;
Matches 64; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

Qy 42 CGAGCTGTCATCTCGCTCATCTGAGTGGCGCGCCGCACTGCAGATGAGCGAGA 101
Db 143 CCGGGCTGTACAGCTTCGCCGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCA 84

Qy 102 TGACCAGCTCCG 154
Db 83 GCGCCACCGCGCGCGCGAGACCGAACCGGTGTACGCGACTGGAGCGGCTTGCCG 31

RESULT 37
ACH91679
ID ACH91679 standard; DNA; 850 BP.
XX
AC ACH91679;
XX
DT 29-JUL-2004 (first entry)
XX
DE Human genome derived single exon probe #24874.
XX
KW Human; probe; ss; gene expression; single exon probe; microarray;
XX
OS Homo sapiens.
XX
PN US2003194704-A1.
XX
PD 16-OCT-2003.
XX
PF 03-APR-2002; 2002US-00029386.
XX
PR 03-APR-2002; 2002US-00029386.
XX
PA (PENN/) PENN S G.
PA (RANK/) RANK D R.
PA (HANZ/) HANZEL D K.
XX
PI Penn SG, Rank DR, Hanzel DK;
XX
DR WPI; 2004-119264/12.
XX
PT New human genome-derived single exon nucleic acid probes useful for human
PT gene expression analysis, for identifying or characterizing alternative
PT splicing events, for assessing genomic alterations or as tools for
PT surveying tissues.
XX
PS Claim 1; SEQ ID NO 24874; 80bp; English.
XX
CC The invention relates to a nucleic acid probe for measuring human gene
CC expression, comprising any of the 27,400 fully defined nucleotide
CC sequences in the specification, or their complements or fragments, and

CC encoding at least 8 amino acids of any of the 6888 amino acid sequences
CC fully defined in the specification. The probe is a single exon probe that
CC hybridises under high stringency conditions to a nucleic acid molecule
CC expressed in human cells or tissues. Also included are a spatially-
CC addressable set of single exon nucleic acid probes for measuring human
CC gene expression (comprising a plurality of single exon nucleic acid
CC probes cited above, where each of the plurality of probes is separately
CC and addressably isolatable or amplifiable from the plurality), a single
CC exon microarray for measuring human gene expression, a method of
CC measuring human gene expression, a vector comprising the single exon
CC probe cited above, an ORF-encoded peptide comprising at least 8
CC contiguous amino acids of any of the above-mentioned amino acid
CC sequences (optionally with conservative amino acid substitutions), an
CC isolated antibody that binds specifically to a peptide cited above,
CC methods of selling and/or licensing single exon probes or microarrays to
CC a customer desiring to measure gene expression, a method of providing
CC human gene expression data by subscription, and a computer-readable
CC storage medium which contains a database having a plurality of records
CC (each record including data on the expression of a single exon probe
CC cited above. The probe, methods and apparatus are useful in gene
CC expression analysis. The probes may be used as tools for surveying
CC tissues to detect the presence of expressed messages that contain their
CC specific exon, or in constructing genome-derived single exon microarrays.
CC In addition, the probes are used in identifying and characterising
CC alternative splicing events, in detecting and characterising gross
CC alterations in the genomic locus that includes their exon, in assessing
CC smaller genomic alterations, in priming the synthesis of nucleic acids,
CC or in expressing the ORF-encoded peptide. The present sequence is a human
CC single exon probe of the invention. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?DocID=20030194704
XX
SQ Sequence 850 BP; 111 A; 291 C; 362 G; 86 T; 0 U; 0 Other;

Query Match 22.7%; Score 35; DB 12; Length 850;
Best Local Similarity 56.5%; Pred. No. 19;
Matches 65; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

Qy 39 GCGCGAGCTGTCATCTCGCTCATCTGAGTGGCGCGCCGCACTGCAGATGAGCGG 98
Db 375 GCGCGAGCGCGCGCGAGTGGCGGACCGCGCACCCAGCCGACGAGGCGCAGG 434

Qy 99 AGATGACCACTCCG 153
Db 435 TCCTGCTGCC 489

RESULT 38
ACH91679/c
ID ACH91679 standard; DNA; 850 BP.
XX
AC ACH91679;
XX
DT 29-JUL-2004 (first entry)
XX
DE Human genome derived single exon probe #24874.
XX
KW Human; probe; ss; gene expression; single exon probe; microarray;
XX
OS Homo sapiens.
XX
PN US2003194704-A1.
XX
PD 16-OCT-2003.
XX
PF 03-APR-2002; 2002US-00029386.
XX
PR 03-APR-2002; 2002US-00029386.
XX
PA (PENN/) PENN S G.
PA (RANK/) RANK D R.

PA (HANZ/) HANZEL D K.

XX	
PI	Penn SG, Rank DR, Hanzel DK;

DR WPI; 2004-119264/12.

PT New human genome-derived single exon nucleic acid probes useful for human
PT gene expression analysis, for identifying or characterizing alternative
PT splicing events, for assessing genomic alterations or as tools for
PT surveying tissues.

PS Claim 1; SEQ ID NO 24874; 80pp; English.

The invention relates to a nucleic acid probe for measuring human gene expression, comprising any of the 27,400 fully defined nucleotide sequences in the specification, or their complements or fragments, and encoding at least 8 aminoacids of any of the 6888 amino acid sequences fully defined in the specification. The probe is a single exon probe that hybridises under high stringency conditions to a nucleic acid molecule expressed in human cells or tissues. Also included are a spatially-addressable set of single exon nucleic acid probes for measuring human gene expression (comprising a plurality of single exon nucleic acid probes cited above, where each of the plurality of probes is separately and addressably isolatable or amplifiable from the plurality), a single exon microarray for measuring human gene expression, a method of measuring human gene expression, a vector comprising the single exon probe cited above, an ORF-encoded peptide comprising at least 8 contiguous amino acids of any of the above-mentioned amino acid sequences (optionally with conservative amino acid substitutions), an isolated antibody that binds specifically to a peptide cited above, methods of selling and/or licensing single exon probes or microarrays to a customer desiring to measure gene expression, a method of providing human gene expression data by subscription, and a computer-readable storage medium which contains a database having a plurality of records (each record including data on the expression of a single exon probe cited above. The probe, methods and apparatus are useful in gene expression analysis. The probes may be used as tools for surveying tissues to detect the presence of expressed messages that contain their specific exon, or in constructing genome-derived single exon microarrays. In addition, the probes are used in identifying and characterising alternative splicing events, in detecting and characterising gross alterations in the genomic locus that includes their exon, in assessing smaller genomic alterations, in priming the synthesis of nucleic acids, or in expressing the ORF-encoded peptide. The present sequence is a human single exon probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html?DocID=20030194704

Sequence 850 BP; 111 A; 291 C; 362 G; 86 T; 0 U; 0 Other;

Query Match	22.7%;	Score 35;	DB 12;	Length 850;
Best Local Similarity	56.5%;	Pred. No. 19;		
Matches	65;	Conservative	0;	Mismatches 50;
				Indels 0;
				Gaps 0;

2 GGC CGAGCTGTCATCTCGCTCATCGTCGAGTCGGCGCCGGAGCTGGTCACTCGCTC 61

489 GGCCGCCGCTGCTCATCGAGCACCCTGGGGCTGGCCGGGGCGCGCGCAGCAGGACTGC 430

62 ATCGTCAGTCGGCGCGCGCCGCGCTGACGATGAGCGAGTACCCAGCTCCGGCC 116
429 GCCCTGCGCTGGGCTGCGGCTGGGTGCGCGGCTGCGCGCACTGGCCCGCCTCCGGCC 375

429 GCCTCTGCGTGGCTGCGGCTGGGTCCGCGGTCCGCCGACTGGCCCGCTCCGGCC 375

RESULT 39
ADP24630

ID ADP24630 standard; cDNA; 1797 BP.

AC ADP24630;

DT 18-NOV-2004 (first entry)

PRO polypeptide encoding cDNA SEQ ID NO:1808.

XX ss; gene; PRO; antiinflammatory; antiarthritic; antirheumatic;
 KW immunosuppressive; osteopathic; antidiabetic; dermatological;
 KW antipsoriatic; antiallergic; antiasthmatic; hepatotropic; respiratory;
 KW gene therapy; immune system.

OS Unidentified.

PN WO2004041170-A2.

PD 21-MAY-2004.

PF 30-OCT-2003; 2003WO-US034312.

PR 01-NOV-2002; 2002US-0423394P.

PA (GETH) GENENTECH INC.

PI Clark H, Schoenfeld J, Van Lookeren M, Williams PM, Wood WJ,
PI Wu TD;

DR WPI; 2004-419628/39.

DR P-PSDB; ADP24631.

PT New PRO polypeptides and polynucleotides, useful for treating e.g.
PT erythematous, rheumatoid arthritis, diabetes mellitus, immune-mediated
PT renal disease, or demyelinating diseases of the central or peripheral
PT nervous system.

PS Claim 1; SEQ ID NO 1808; 2940pp; English.

The invention relates to a novel isolated nucleic acid and the PRO polypeptide encoded by it. A protein of the invention has antiinflammatory, antiarthritic, antirheumatic, immunosuppressive, osteoplastic, antidiabetic, dermatological, antipsoriatic, antiallergic, antiasthmatic, hepatotropic, and respiratory activity. A polynucleotide of the invention may have a use in gene therapy. The PRO polypeptide, its agonist, antagonist, or antibody that specifically binds to the polypeptide is useful for treating an immune related disorder such as systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an idiopathic inflammatory myopathy, Sjogren's syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, a demyelinating disease of the central or peripheral nervous system, idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome, a chronic inflammatory demyelinating polyneuropathy, a hepatobiliary disease, infectious or autoimmune chronic active hepatitis, primary biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis, inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's disease, an autoimmune or immune-mediated enteropathy, whipple's disease, an autoimmune or immune-mediated skin disease, a bulous skin disease, erythema multiforme, contact dermatitis, psoriasis, an allergic disease, asthma, allergic rhinitis, atopic dermatitis, food hypersensitivity, urticaria, an immunologic disease of the lung, eosinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity pneumonitis, a transplantation associated disease, graft rejection or graft-versus-host disease. The present sequence encodes a PRO protein of the invention.

Sequence 1797 BP; 263 A; 645 C; 552 G; 337 T; 0 U; 0 Other;

Query Match	22.7%;	Score 35;	DB 13;	Length 1797;
Best Local Similarity	56.5%;	Pred. No. 20;		
Matches	65;	Conservative	0;	Mismatches 50;
				Indels 0;
				Gaps 0

2 GGGCGAGCTGTCATCTCGCTCATCGAGTCGGCGCCGGAGCTGTCATCTCGCTC 61

597 GGGCGCGCTGCTCATCGAGCACTGGGGCTGGCGCGCGCGCGCGAGCAGGACTGC 656

62 ATCGTCAGTCCGGCCGGCCGACTCGACGATGAGCGAGATGACCACTCCGGCC 116

657 GCGTCTGGGCTGGGTCCCGGTCCCGCACTGGCCGCTCCGCC 711

RESULT 40
ADP24630/c
ID ADP24630 standard; cDNA; 1797 BP.
XX
XX ADP24630;
AC
XX
DT 18-NOV-2004 (first entry)
XX
DE PRO polypeptide encoding cDNA SEQ ID NO:1808.
XX
KW ss; gene; PRO; antiinflammatory; antiarthritic; antirheumatic;
KW immunosuppressive; osteopathic; antidiabetic; dermatological;
KW antipsoriatic; antiallergic; antiasthmatic; hepatotropic; respiratory;
KW gene therapy; immune system.
XX
OS Unidentified.
XX
PN WO2004041170-A2.
XX
PD 21-MAY-2004.
XX
PF 30-OCT-2003; 2003WO-US034312.
XX
PR 01-NOV-2002; 2002US-0423394P.
XX
PA (GETH) GENENTECH INC.
XX
PI Clark H, Schoenfeld J, Van Lookeren M, Williams PM, Wood WI,
PI Wu TD;
XX
DR WPI; 2004-419628/39.
DR P-PSDB; ADP24631.
XX
PT New PRO polypeptides and polynucleotides, useful for treating e.g.
PT erythematous, rheumatoid arthritis, diabetes mellitus, immune-mediated
PT renal disease, or demyelinating diseases of the central or peripheral
PT nervous system.
XX
PS Claim 1; SEQ ID NO 1808; 2940pp; English.
XX
CC The invention relates to a novel isolated nucleic acid and the PRO
CC polypeptide encoded by it. A protein of the invention has
CC antiinflammatory, antiarthritic, antirheumatic, immunosuppressive,
CC osteopathic, antidiabetic, dermatological, antipsoriatic, antiallergic,
CC antiasthmatic, hepatotropic, and respiratory activity. A polynucleotide
CC of the invention may have a use in gene therapy. The PRO polypeptide, its
CC agonist, antagonist, or antibody that specifically binds to the
CC polypeptide is useful for treating an immune related disorder such as
CC systemic lupus erythematous, rheumatoid arthritis, osteoarthritis,
CC juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an
CC idiopathic inflammatory myopathy, Sjogren's syndrome, systemic
CC vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune
CC thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal
CC disease, a demyelinating disease of the central or peripheral nervous
CC system, idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome,
CC a chronic inflammatory demyelinating polyneuropathy, a hepatobiliary
CC disease, infectious or autoimmune chronic active hepatitis, primary
CC biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis,
CC inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's
CC disease, an autoimmune or immune-mediated skin disease, a bulous skin
CC disease, erythema multiforme, contact dermatitis, psoriasis, an allergic
CC disease, asthma, allergic rhinitis, atopic dermatitis, food
CC hypersensitivity, urticaria, an immunologic disease of the lung,
CC eosinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity
CC pneumonitis, a transplantation associated disease, graft rejection or
CC graft-versus-host disease. The present sequence encodes a PRO protein of
CC the invention.
XX
SQ Sequence 1797 BP; 263 A; 645 C; 552 G; 337 T; 0 U; 0 Other;

Query Match 22.7%; Score 35; DB 13; Length 1797;
Best Local Similarity 56.5%; Pred. No. 20;

Matches 65; Conservative 0; Mismatches 50; Indels 0; Gaps 0;
QY 39 GGCCGAGCTGTCATCTCGTCATCGAGTCGCGCCGCCGACTCGAGTAGCG 98
DB 711 GGCCGAGCGCGCCAGTCGCGCGACCGGACCCAGCCGACGAGGCGCAGG 652
QY 99 AGATGACCACTCCGCGCCGCGACTCGAGTAGCGAGTAGACGACTCCGCC 153
DB 651 TCCTGCTCGCGCGCGCCGCCGCGCCAGCCAGGTGCTGATGAGACGCGGCC 597

RESULT 41
AAS18438
ID AAS18438 standard; DNA; 1681 BP.
XX
XX AAS18438;
AC
XX
DT 12-MAR-2002 (first entry)
XX
DE Contig 115 DNA encoding S. narbonensis polyketide synthase.
XX
KW Narbonolide polyketide synthase; PKS; narbomycin modification enzyme;
KW erythromycin; rapamycin; tylosin; picromycin; methylmycin; neomethylmycin;
KW agriculture; ds.
XX
OS Streptomyces narbonensis.
XX
PN US6303767-B1.
XX
PD 16-OCT-2001.
XX
PF 05-NOV-1999; 99US-00434288.
XX
PR 05-NOV-1998; 98US-0107093P.
PR 27-MAY-1999; 99US-00320878.
XX
PA (KOSA-) KOSAN BIOSCIENCES INC.
XX
PI Beclach MC, McDaniel R;
PI
XX
DR WPI; 2002-065495/09.
XX
PT Nucleic acids encoding narbonolide polyketide synthases from Streptomyces
PT narbonensis, useful for the recombinant production of polyketides, e.g.
PT narbomycin.
XX
PS Claim 1; Col 18; 24pp; English.
XX
CC The present invention relates to recombinant DNA vectors (cosmids) that
CC encode for the narbonolide polyketide synthase (PKS) enzyme and various
CC narbomycin modification enzymes from Streptomyces narbonensis. The
CC recombinant DNA vectors can be used to produce recombinant ketide
CC synthases and a variety of different polyketides (e.g. erythromycin,
CC rapamycin, tylosin, narbomycin, picromycin, methylmycin and
CC neomethylmycin) for use in agriculture, medicine and health. The
CC recombinant vectors may be used to produce polyketides in relatively high
CC yields. AAS18432-AAS18443 represent contig DNA sequences that encode for
CC S. narbonensis PKS enzymes
XX
SQ Sequence 1681 BP; 231 A; 672 C; 580 G; 198 T; 0 U; 0 Other;

Query Match 22.6%; Score 34.8; DB 6; Length 1681;
Best Local Similarity 55.9%; Pred. No. 22;
Matches 66; Conservative 0; Mismatches 52; Indels 0; Gaps 0;
QY 1 CGCCGAGCTGTCATCTCGTCATCGTCGAGTCGCGCGCCGAGAGTCATCTCGCT 60
DB 424 CTGGCGCGCTGCTCAGCGGGCTACCCGCGGTGCGGGCGGGCGGCTTCGGTCCGC 483
QY 61 CATCTGAGTCGCGCGCGCGCGACTCGAGTCAGCGAGTAGACGACTCCGCCGC 118
DB 484 CGCCGAGGCGCGCGCGCGCGACCGGCGAGGAGGAGGACCTTGCGGCGCGCGC 541

```

RESULT 42
AAS18438/C
ID AAS18438 standard; DNA; 1681 BP.
XX
XX AAS18438;
AC
XX
XX 12-MAR-2002 (first entry)
XX
XX Contig 115 DNA encoding S. narbonensis polyketide synthase.
DE
XX
XX Narbonolide polyketide synthase; PKS; narbomycin modification enzyme;
KW erythromycin; rapamycin; tylosin; picromycin; methylmycin; neomethymycin;
KW agriculture; ds.
XX
XX Streptomyces narbonensis.
OS
XX
XX US6303767-B1.
PN
XX
XX 16-OCT-2001.
PD
XX
XX 05-NOV-1999; 99US-00434288.
PF
XX
XX 05-NOV-1998; 98US-0107093P.
PR
XX 27-MAY-1999; 99US-00320878.
PR
XX
XX (KOSA-) KOSAN BIOSCIENCES INC.
PA
XX
XX Betlach MC, Mcdaniel R;
PI
XX
XX WPI; 2002-065495/09.
DR
XX
XX Nucleic acids encoding narbonolide polyketide synthases from Streptomyces
PT narbonensis, useful for the recombinant production of polyketides, e.g.
PT narbomycin.
XX
XX
XX Claim 1; Col 18; 24pp; English.
PS
XX
XX
XX The present invention relates to recombinant DNA vectors (cosmids) that
CC encode for the narbonolide polyketide synthase (PKS) enzyme and various
CC narbomycin modification enzymes from Streptomyces narbonensis. The
CC recombinant DNA vectors can be used to produce recombinant ketide
CC synthases and a variety of different polyketides (e.g. erythromycin,
CC rapamycin, tylosin, narbomycin, picromycin, methylmycin and
CC neomethymycin) for use in agriculture, medicine and health. The
CC recombinant vectors may be used to produce polyketides in relatively high
CC yields. AAS18432-AAS18443 represent contig DNA sequences that encode for
CC S. narbonensis PKS enzymes
CC
XX
SQ Sequence 1681 BP; 231 A; 672 C; 580 G; 198 T; 0 U; 0 Other;

Query Match 22.6%; Score 34.8; DB 6; Length 1681;
Best Local Similarity 55.9%; Pred. No. 22;
Matches 66; Conservative 0; Mismatches 52; Indels 0; Gaps 0

QY 37 GCGGCCGAGCTGTCATCTCGTCATTCGAGTCGCGCGCCGCCGACTCGACGATGAG 96
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 541 GCCGCCCGCCAGGTCCCTCTCCGCTGGCCGGTGCTGCCGTTCGGCGGCCCTGCGCGGC 482
| | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 97 CGAGATGACCAAGCTCCGCGCCGCCGACTCGACGATGACGACGATGACCAAGCTCCGCGCG 154
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 481 CGACCGGAGCGCCCGCGCGCCGCCGACCCGCGGAGTGAAGCCCGCTGAGCAGCGCGCCAG 424
| | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 43
ADL91894
ID ADL91894 standard; DNA; 1681 BP.
XX
XX ADL91894;
AC
XX
XX 20-MAY-2004 (first entry)
DT
XX
XX Streptomyces narbonolide polyketide synthase coding sequence #7.
DE

```

XX		narbonolide polyketide synthase gene; polyhydroxyalkanoate monomer;
KW		medical application; industrial application; ds.
OS		Streptomyces narbonensis.
PN	US2003194784-AI.	
PD	16-OCT-2003.	
PF	15-OCT-2002; 2002US-00271889.	
PR	17-APR-2001; 2001US-00836821.	
PR	18-MAY-2001; 2001US-00860846.	
XX	18-MAY-2001; 2001US-00861289.	
PA	(SHER/) SHERMAN D H.	
PA	(LIUH/) LIU H.	
PA	(XUEY/) XUE Y.	
PA	(ZHAO/) ZHAO L.	
PI	Sherman DH, Liu H, Xue Y, Zhao L;	
DR	WPI; 2004-119267/12.	
PT	New isolated nucleic acid comprising a narbonolide polyketide synthase gene from Streptomyces narbonensis, useful for providing a polyhydroxyalkanoate monomer for medical and industrial applications.	
PS	Claim 1; SEQ ID NO 7; 362pp; English.	
CC	The invention comprises coding sequences for the narbonolide polyketide synthase gene from Streptomyces narbonensis. The DNA sequence of the invention are useful for providing polyhydroxyalkanoate monomer for medical and industrial applications. The present DNA sequence represents a Streptomyces narbonensis narbonolide polyketide synthase coding sequence of the invention.	
SQ	Sequence 1681 BP; 231 A; 672 C; 580 G; 198 T; 0 U; 0 Other;	
Dq	Query Match 22.6%; Score 34.8; DB 12; Length 1681; Best Local Similarity 55.9%; Pred. No. 22; Matches 66; Conservative 0; Mismatches 52; Indels 0; Gaps 0,	
Dd	CGGCCGAGCTGTGCATCTCCTCATTCGTGAGTGGCGCCGAGACTGTGCATCTGCT 60	
	424 CTGCGCGCGTGCTCAAGCGGGCTCACCGCGGTGCGGGCGCGCGCTCCGGTCGGC 483	
Dy	61 CATCGTAGTCGGCGCGCGCGGAACCTGACGATGAGCGAATGACCAGCTCCGCCCC 118	
Dz	484 CGCGCGAGGGCGCGCGCGGACCGGCGGCGGAGAGGAACTGGGCGGCGGC 541	
ID	ADL91894 standard; DNA; 1681 BP.	
DE	RESULT 44	
DD	ADL91894/c	
DN	ADL91894;	
DT	20-MAY-2004 (first entry)	
DS	Streptomyces narbonolide polyketide synthase coding sequence #7.	
KM	narbonolide polyketide synthase gene; polyhydroxyalkanoate monomer;	
KW	medical application; industrial application; ds.	
OS	Streptomyces narbonensis.	
PN	US2003194784-AI.	
PD	16-OCT-2003.	
PF	15-OCT-2002; 2002US-00271889.	
PR	17-APR-2001; 2001US-00836821.	
PR	18-MAY-2001; 2001US-00860846.	
XX	18-MAY-2001; 2001US-00861289.	
PA	(SHER/) SHERMAN D H.	
PA	(LIUH/) LIU H.	
PA	(XUEY/) XUE Y.	
PA	(ZHAO/) ZHAO L.	
PI	Sherman DH, Liu H, Xue Y, Zhao L;	
DR	WPI; 2004-119267/12.	
PT	New isolated nucleic acid comprising a narbonolide polyketide synthase gene from Streptomyces narbonensis, useful for providing a polyhydroxyalkanoate monomer for medical and industrial applications.	
PS	Claim 1; SEQ ID NO 7; 362pp; English.	
CC	The invention comprises coding sequences for the narbonolide polyketide synthase gene from Streptomyces narbonensis. The DNA sequence of the invention are useful for providing polyhydroxyalkanoate monomer for medical and industrial applications. The present DNA sequence represents a Streptomyces narbonensis narbonolide polyketide synthase coding sequence of the invention.	
SQ	Sequence 1681 BP; 231 A; 672 C; 580 G; 198 T; 0 U; 0 Other;	
Dq	Query Match 22.6%; Score 34.8; DB 12; Length 1681; Best Local Similarity 55.9%; Pred. No. 22; Matches 66; Conservative 0; Mismatches 52; Indels 0; Gaps 0,	
Dd	CGGCCGAGCTGTGCATCTCCTCATTCGTGAGTGGCGCCGAGACTGTGCATCTGCT 60	
	424 CTGCGCGCGTGCTCAAGCGGGCTCACCGCGGTGCGGGCGCGCGCTCCGGTCGGC 483	
Dy	61 CATCGTAGTCGGCGCGCGCGGAACCTGACGATGAGCGAATGACCAGCTCCGCCCC 118	
Dz	484 CGCGCGAGGGCGCGCGCGGACCGGCGGCGGAGAGGAACTGGGCGGCGGC 541	
ID	ADL91894 standard; DNA; 1681 BP.	
DE	RESULT 44	
DD	ADL91894/c	
DN	ADL91894;	
DT	20-MAY-2004 (first entry)	
DS	Streptomyces narbonolide polyketide synthase coding sequence #7.	
KM	narbonolide polyketide synthase gene; polyhydroxyalkanoate monomer;	
KW	medical application; industrial application; ds.	
OS	Streptomyces narbonensis.	
PN	US2003194784-AI.	
PD	16-OCT-2003.	
PF	15-OCT-2002; 2002US-00271889.	
PR	17-APR-2001; 2001US-00836821.	
PR	18-MAY-2001; 2001US-00860846.	
XX	18-MAY-2001; 2001US-00861289.	
PA	(SHER/) SHERMAN D H.	
PA	(LIUH/) LIU H.	
PA	(XUEY/) XUE Y.	
PA	(ZHAO/) ZHAO L.	
PI	Sherman DH, Liu H, Xue Y, Zhao L;	
DR	WPI; 2004-119267/12.	
PT	New isolated nucleic acid comprising a narbonolide polyketide synthase gene from Streptomyces narbonensis, useful for providing a polyhydroxyalkanoate monomer for medical and industrial applications.	
PS	Claim 1; SEQ ID NO 7; 362pp; English.	
CC	The invention comprises coding sequences for the narbonolide polyketide synthase gene from Streptomyces narbonensis. The DNA sequence of the invention are useful for providing polyhydroxyalkanoate monomer for medical and industrial applications. The present DNA sequence represents a Streptomyces narbonensis narbonolide polyketide synthase coding sequence of the invention.	
SQ	Sequence 1681 BP; 231 A; 672 C; 580 G; 198 T; 0 U; 0 Other;	

XX 17-APR-2001; 2001US-00836821.
PR 18-MAY-2001; 2001US-00860846.
PR 18-MAY-2001; 2001US-00861289.
XX
PA (SHER/) SHERMAN D H.
PA (LIUH/) LIU H.
PA (XUEY/) XUE Y.
PA (ZHAO/) ZHAO L.
XX
PI Sherman DH, Liu H, Xue Y, Zhao L;
XX
DR WPI; 2004-119267/12.
XX
PT New isolated nucleic acid comprising a narbonolide polyketide synthase
PT gene from Streptomyces narbonensis, useful for providing a
PT polyhydroxyalkanoate monomer for medical and industrial applications.
XX
PS Claim 1; SEQ ID NO 7; 362pp; English.
XX
CC The invention comprises coding sequences for the narbonolide polyketide
CC synthase gene from Streptomyces narbonensis. The DNA sequence of the
CC invention are useful for providing polyhydroxyalkanoate monomer for
CC medical and industrial applications. The present DNA sequence represents
CC a Streptomyces narbonensis narbonolide polyketide synthase coding
CC sequence of the invention.
XX
SQ Sequence 1681 BP; 231 A; 672 C; 580 G; 198 T; 0 U; 0 Other;

Query Match 22.6%; Score 34.8; DB 12; Length 1681;
Best Local Similarity 55.9%; Pred. No. 22;
Matches 66; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

QY 37 GCGGCCGAGCTGTCATCTCGCTCATCTGAGTCGGCGCCCGACTCGACGATGAG 96
DB 541 GCCGCCCGCCAGGTCCCTCTCCGCTGGCCGGTGCCTCGCGCGGCCCTGCGCGGC 482

QY 97 CGAGATGACCACTCCGGCGCCGACTCGACGATGAGCGAGATGACCACTCCGGCGC 154
DB 481 CGACCGGAGCGCCGCGCGCGCGCGCGCGGTGAGCCCGCTGAGCAGCGCGCGCAG 424

RESULT 45
AAS59803
ID AAS59803 standard; DNA; 1498 BP.
XX
AC AAS59803;
XX
DT 13-FEB-2002 (first entry)
XX
DE Propionibacterium acnes immunogenic protein encoding DNA #298.
XX
KW SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
KW dermatological; osteopathic; neuroprotectant; ds.
XX
OS Propionibacterium acnes.
XX
PN WO200181581-A2.
XX
PD 01-NOV-2001.
XX
PF 20-APR-2001; 2001WO-US012865.
XX
PR 21-APR-2000; 2000US-0199047P.
PR 02-JUN-2000; 2000US-0208841P.
PR 07-JUL-2000; 2000US-0216747P.
XX
PA (CORI-) CORIXA CORP.
XX
PI Skeiky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;
PI L'maisonneuve J, Zhang Y, Jen S, Carter D;

XX
DR WPI; 2001-616774/71.
XX
PT Propionibacterium acnes polypeptides and nucleic acids useful for
PT vaccinating against and diagnosing infections, especially useful for
PT treating acne vulgaris.
XX
PS Claim 1; SEQ ID NO 298; 1069pp; English.
XX
CC Sequences AAS59506-AAS59804 represent DNA molecules encoding
CC Propionibacterium acnes immunogenic polypeptides. The proteins and their
CC associated DNA sequences are used in the treatment, prevention and
CC diagnosis of medical conditions caused by P. acnes. The disorders include
CC SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and
CC osteomyelitis), uveitis and endophthalmitis. P. acnes is also involved in
CC infections of bone, joints and the central nervous system, however it is
CC particularly involved in the inflammatory lesions associated with acne
CC vulgaris. A method for detecting the presence or absence of P. acnes in a
CC patient comprises contacting a sample with a binding agent that binds to
CC the proteins of the invention and determining the amount of bound protein
CC in the sample. The polypeptides may be used as antigens in the production
CC of antibodies specific for P. acnes proteins. These antibodies can be
CC used to downregulate expression and activity of P. acnes polypeptides and
CC therefore treat P. acnes infections. The antibodies may also be used as
CC diagnostic agents for determining P. acnes presence, for example, by
CC enzyme linked immunosorbent assay (ELISA). This sequence encodes the
CC polypeptides shown in AAU67430-AAU67444 and AAU68011-AAU68015. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1498 BP; 286 A; 458 C; 450 G; 301 T; 0 U; 3 Other;

Query Match 22.5%; Score 34.6; DB 4; Length 1498;
Best Local Similarity 56.6%; Pred. No. 25;
Matches 64; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

QY 30 CGAGTCGGCGCGCGAGCTGTCATCTCGCTCATCTGAGTCGGCGCGCGGACTCGA 89
DB 696 CCACTGCGAGCTGCGCGCGGATCCGCTGCTCTCACTCACTATCAACCAACCACC 755

QY 90 CGATGACGAGATGACCACTCCGGCGCGCGGACTCGACGATGAGCGGATGAC 142
DB 756 TGGTGAAGGAGAAGACCCGTACCCCGGCGGAGACTGTCGTGAGGCTGTGAC 808

Search completed: April 8, 2005, 23:27:00
Job time : 442 secs

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OM nucleic - nucleic search, using sw model.

Run on: April 8, 2005, 21:45:05 ; Search time 1885 Seconds
(without alignments)
3958.675 Million cell updates/sec

Title: US-09-887-194A-13

Perfect score: 154

Sequence: 1 cggcgcgagctgtcatctc.....gagatgaccagctccgcgcg 154

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : GenEmbl:*

- 1: gb_ba:*
- 2: gb_htg:*
- 3: gb_in:*
- 4: gb_cm:*
- 5: gb_ov:*
- 6: gb_pat:*
- 7: gb_ph:*
- 8: gb_pl:*
- 9: gb_pr:*
- 10: gb_ro:*
- 11: gb_sts:*
- 12: gb_sy:*
- 13: gb_un:*
- 14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	154	100.0	154	6	AX367128 Sequence
2	154	100.0	154	6	AX367128 Sequence
3	154	100.0	154	6	AX392336 Sequence
4	154	100.0	154	6	AX392336 Sequence
5	112	72.7	4974	6	AX353724 Sequence
6	112	72.7	4974	6	AX353724 Sequence
7	82.8	53.8	6611	6	AX392337 Sequence
8	82.8	53.8	6611	6	AX392337 Sequence
9	81	52.6	963	6	AX367144 Sequence
10	81	52.6	963	6	AX367144 Sequence
11	80	51.9	80	6	AX367127 Sequence
12	80	51.9	80	6	AX367127 Sequence
13	80	51.9	80	6	AX392335 Sequence
14	80	51.9	80	6	AX392335 Sequence
15	80	51.9	92	6	AX367129 Sequence
16	80	51.9	92	6	AX367129 Sequence
17	45.8	29.7	1717	6	AX367139 Sequence
18	45.8	29.7	1717	6	AX367139 Sequence
19	41.8	27.1	13802	1	STB579650 Streptomy

C	20	41.8	27.1	13802	1	STB579650	AJ579650 Streptomy
C	21	38.6	25.1	110000	1	BX571966_08	Continuation (9 of
C	22	38.6	25.1	110000	1	BX571966_08	Continuation (9 of
C	23	38.2	24.8	10348	1	AE004846	AE004846 Pseudomon
C	24	38.2	24.8	10348	1	AE004846	AE004846 Pseudomon
C	25	38	24.7	301925	1	AP005046	AP005046 Streptomy
C	26	38	24.7	301925	1	AP005046	AP005046 Streptomy
C	27	37	24.0	148829	8	AC134925	AC134925 Oryza sat
C	28	37	24.0	148829	8	AC134925	AC134925 Oryza sat
C	29	36.8	23.9	110000	1	AP006618_59	Continuation (60 o
C	30	36.8	23.9	110000	1	AP006618_59	Continuation (60 o
C	31	36.6	23.8	110000	1	AE016822_14	Continuation (15 o
C	32	36.6	23.8	110000	1	AE016822_14	Continuation (15 o
C	33	36.6	23.8	349315	1	BX572593	BX572593 Rhodopsu
C	34	36.6	23.8	349315	1	BX572593	BX572593 Rhodopsu
C	35	36.4	23.6	674	8	AK063727	AK063727 Oryza sat
C	36	36.4	23.6	674	8	AK063727	AK063727 Oryza sat
C	37	36.4	23.6	133449	8	AC107207	AC107207 Oryza sat
C	38	36.4	23.6	133449	8	AC107207	AC107207 Oryza sat
C	39	36.4	23.6	150743	8	AC133450	AC133450 Oryza sat
C	40	36.4	23.6	150743	8	AC133450	AC133450 Oryza sat
C	41	36.2	23.5	8973	1	AY081837	AY081837 Bradyrhiz
C	42	36.2	23.5	8973	1	AY081837	AY081837 Bradyrhiz
C	43	36.2	23.5	123169	9	AC008771	AC008771 Homo sapi
C	44	36.2	23.5	123169	9	AC008771	AC008771 Homo sapi
C	45	36.2	23.5	126052	9	AC018764	AC018764 Homo sapi
C	46	36.2	23.5	126052	9	AC018764	AC018764 Homo sapi
C	47	36.2	23.5	298550	1	AP005961	AP005961 Bradyrhiz
C	48	36.2	23.5	298550	1	AP005961	AP005961 Bradyrhiz
C	49	36	23.4	129647	8	AC097280	AC097280 Oryza sat
C	50	36	23.4	129647	8	AC097280	AC097280 Oryza sat
C	51	36	23.4	190050	1	AL646059	AL646059 Ralstonia
C	52	36	23.4	190050	1	AL646059	AL646059 Ralstonia
C	53	36	23.4	344805	1	BX640434	BX640434 Bordetell
C	54	36	23.4	344805	1	BX640434	BX640434 Bordetell
C	55	36	23.4	348074	1	BX640449	BX640449 Bordetell
C	56	36	23.4	348074	1	BX640449	BX640449 Bordetell
C	57	35.8	23.2	1044	8	AK108311	AK108311 Oryza sat
C	58	35.8	23.2	1044	8	AK108311	AK108311 Oryza sat
C	59	35.8	23.2	1102	8	HVMTB2	X70876 H.vulgare m
C	60	35.8	23.2	1102	8	HVMTB2	X70876 H.vulgare m
C	61	35.8	23.2	180186	8	AP003104	AP003104 Oryza sat
C	62	35.8	23.2	180186	8	AP003104	AP003104 Oryza sat
C	63	35.8	23.2	283100	1	SCO939110	AL939110 Streptomy
C	64	35.8	23.2	283100	1	SCO939110	AL939110 Streptomy
C	65	35.6	23.1	103788	8	AP004747	AP004747 Oryza sat
C	66	35.6	23.1	103788	8	AP004747	AP004747 Oryza sat
C	67	35.6	23.1	119290	8	AP005300	AP005300 Oryza sat
C	68	35.6	23.1	119290	8	AP005300	AP005300 Oryza sat
C	69	35.6	23.1	278492	1	BX248347	BX248347 Mycobacte
C	70	35.6	23.1	278492	1	BX248347	BX248347 Mycobacte
C	71	35.6	23.1	302178	1	AE016918	AE016918 Chromobac
C	72	35.6	23.1	302178	1	AE016918	AE016918 Chromobac
C	73	35.6	23.1	340900	1	SME591791	AL591791 Sinorhizo
C	74	35.6	23.1	340900	1	SME591791	AL591791 Sinorhizo
C	75	35.2	22.9	325483	1	AP005050	AP005050 Streptomy
C	76	35.2	22.9	325483	1	AP005050	AP005050 Streptomy
C	77	35	22.7	1020	9	AB078417	AB078417 Homo sapi
C	78	35	22.7	1020	9	AB078417	AB078417 Homo sapi
C	79	35	22.7	1797	9	AF438313	AF438313 Homo sapi
C	80	35	22.7	1797	9	AF438313	AF438313 Homo sapi
C	81	35	22.7	223542	9	AC006515	AC006515 Homo sapi
C	82	35	22.7	223542	9	AC006515	AC006515 Homo sapi
C	83	35	22.7	302174	1	AE017241	AE017241 Mycobacte
C	84	35	22.7	302174	1	AE017241	AE017241 Mycobacte
C	85	34.8	22.6	1681	6	ARI73228	ARI73228 Sequence
C	86	34.8	22.6	1681	6	ARI73228	ARI73228 Sequence
C	87	34.8	22.6	12425	1	AE005093	AE005093 Halobacte
C	88	34.8	22.6	12425	1	AE005093	AE005093 Halobacte
C	89	34.8	22.6	110000	1	CP000011_00	CP000011 Burkholde
C	90	34.8	22.6	110000	1	CP000011_00	CP000011 Burkholde
C	91	34.8	22.6	299925	1	AP005043	AP005043 Streptomy
C	92	34.8	22.6	299925	1	AP005043	AP005043 Streptomy

93	34.6	22.5	810	8	AKI05166	AKI05166	Oryza sat
C	94	34.6	22.5	810	8	AKI05166	Oryza sat
C	95	34.6	22.5	1498	6	CQ364015	Sequence
C	96	34.6	22.5	1498	6	CQ364015	Sequence
C	97	34.6	22.5	6422	6	CQ363867	Sequence
C	98	34.6	22.5	6422	6	CQ363867	Sequence
C	99	34.6	22.5	11384	1	AE012519	Xanthomon
C	100	34.6	22.5	11384	1	AE012519	Xanthomon

ALIGNMENTS

RESULT 1
AX367128
LOCUS AX367128 154 bp DNA linear PAT 16-FEB-2002
DEFINITION Sequence 13 from Patent WO0200904.
ACCESSION AX367128
VERSION AX367128.1 GI:18855329
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Glassman,K.F., Gordon-Kamm,W.J., Kinney,A.J., Lowe,K., Stecca,K.L.
TITLE Recombinant constructs and their use in reducing gene expression
JOURNAL Patent: WO 0200904-A 13 03-JAN-2002;
E. I. du Pont de Nemours and Company (US) ; PIONEER HI-BRED
INTERNATIONAL, INC. (US)
FEATURES
Source
1. .154
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="ELVISLIVES complementary region of PKS133"

ORIGIN
Query Match 100.0%; Score 154; DB 6; Length 154;
Best Local Similarity 100.0%; Pred. No. 1.1e-19;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	CGGCCGAGCTGTCATCTCGCTCATCTGAGTCCGGCCGAGAGCTGTCTCTCGCT	60
Db	1	CGGCCGAGCTGTCATCTCGCTCATCTGAGTCCGGCCGAGAGCTGTCTCTCGCT	60
QY	61	CATCGTCGAGTCGGCGCCGCCGACTCGACGATGAGCGAGATGACCAAGCTCCGGCCGCG	120
Db	61	CATCGTCGAGTCGGCGCCGCCGACTCGACGATGAGCGAGATGACCAAGCTCCGGCCGCG	120
QY	121	ACTCGACGATGAGCGAGATGACCAAGCTCCGGCCG	154
Db	121	ACTCGACGATGAGCGAGATGACCAAGCTCCGGCCG	154

RESULT 2

AX367128/c
LOCUS AX367128 154 bp DNA linear PAT 16-FEB-2002
DEFINITION Sequence 13 from Patent WO0200904.
ACCESSION AX367128
VERSION AX367128.1 GI:18855329
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Glassman,K.F., Gordon-Kamm,W.J., Kinney,A.J., Lowe,K., Stecca,K.L.
TITLE Recombinant constructs and their use in reducing gene expression
JOURNAL Patent: WO 0200904-A 13 03-JAN-2002;
E. I. du Pont de Nemours and Company (US) ; PIONEER HI-BRED
INTERNATIONAL, INC. (US)
FEATURES
Location/Qualifiers

FEATURES

source

1. .154
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="ELVISLIVES complementary region of PKS133"

Query Match 100.0%; Score 154; DB 6; Length 154;
Best Local Similarity 100.0%; Pred. No. 1.1e-19;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	CGGCCGAGCTGTCATCTCGCTCATCTGAGTCCGGCCGAGAGCTGTCTCTCGCT	60
Db	154	CGGCCGAGCTGTCATCTCGCTCATCTGAGTCCGGCCGAGAGCTGTCTCTCGCT	95
QY	61	CATCGTCGAGTCGGCGCCGCCGACTCGACGATGAGCGAGATGACCAAGCTCCGGCCGCG	120
Db	94	CATCGTCGAGTCGGCGCCGCCGACTCGACGATGAGCGAGATGACCAAGCTCCGGCCGCG	35
QY	121	ACTCGACGATGAGCGAGATGACCAAGCTCCGGCCG	154
Db	34	ACTCGACGATGAGCGAGATGACCAAGCTCCGGCCG	1

RESULT 3
AX392336
LOCUS AX392336 154 bp DNA linear PAT 23-MAR-2002
DEFINITION Sequence 25 from Patent WO0216565.
ACCESSION AX392336
VERSION AX392336.1 GI:19700689
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Booth,J.R., Cahoon,R.E., Hiltz,W.D., Kinney,A.J. and Yadav,N.S.
TITLE Nucleotide sequences of a new class of diverged delta-9
JOURNAL Patent: WO 0216565-A 25 28-FEB-2002;
E. I. du Pont de Nemours and Company (US)
FEATURES
Source
1. .154
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="ELVISLIVES complementary region of PKS133"

ORIGIN

Query Match 100.0%; Score 154; DB 6; Length 154;
Best Local Similarity 100.0%; Pred. No. 1.1e-19;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	CGGCCGAGCTGTCATCTCGCTCATCTGAGTCCGGCCGAGAGCTGTCTCTCGCT	60
Db	1	CGGCCGAGCTGTCATCTCGCTCATCTGAGTCCGGCCGAGAGCTGTCTCTCGCT	60
QY	61	CATCGTCGAGTCGGCGCCGCCGACTCGACGATGAGCGAGATGACCAAGCTCCGGCCGCG	120
Db	61	CATCGTCGAGTCGGCGCCGCCGACTCGACGATGAGCGAGATGACCAAGCTCCGGCCGCG	120
QY	121	ACTCGACGATGAGCGAGATGACCAAGCTCCGGCCG	154
Db	121	ACTCGACGATGAGCGAGATGACCAAGCTCCGGCCG	154

RESULT 4

AX392336/c
LOCUS AX392336 154 bp DNA linear PAT 23-MAR-2002
DEFINITION Sequence 25 from Patent WO0216565.
ACCESSION AX392336
VERSION AX392336.1 GI:19700689
KEYWORDS
SOURCE synthetic construct

FEATURES

ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Booth,J.R., Cahoon,R.E., Hiltz,W.D., Kinney,A.J. and Yadav,N.S.
TITLE Nucleotide sequences of a new class of diverged delta-9
JOURNAL stearoyl-acp desaturase genes
Patent: WO 0216565-A 25 28-FEB-2002;
E.I. du Pont de Nemours and Company (US)
FEATURES Location/Qualifiers
source 1..154
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="ELVISLIVES complementary region of pKS133"
ORIGIN
Query Match 100.0%; Score 154; DB 6; Length 154;
Best Local Similarity 100.0%; Pred. No. 1.1e-19;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGGCCGAGCTGGTCACTCTCGCTCATGTCGAGTCGCGCGCGGAGCTGTGTCATCTCGCT 60
DB 154 CGGCCGAGCTGGTCACTCTCGCTCATGTCGAGTCGCGCGCGGAGCTGTGTCATCTCGCT 95
QY 61 CATCGTCGAGTCGCGCGCGCGCGGAGTCGAGTCGAGCGAGATGACCACTCCGCGCGCG 120
DB 94 CATCGTCGAGTCGCGCGCGCGCGGAGTCGAGTCGAGCGAGATGACCACTCCGCGCGCG 35
QY 121 ACTCGACGATGAGCGAGATGACCACTCCGCGCG 154
DB 34 ACTCGACGATGAGCGAGATGACCACTCCGCGCG 1
RESULT 5
AX353724 4974 bp DNA linear PAT 06-FEB-2002
LOCUS Sequence 17 from Patent EP1174510.
DEFINITION AX353724
ACCESSION AX353724
VERSION AX353724.1 GI:18618779
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Allen,S.M., Butler,K.H., Carlson,T.J. and Ilag,L.L.
TITLE Plasmidial phosphoglucomutase genes
JOURNAL Patent: EP 1174510-A 17 23-JAN-2002;
E.I. du Pont de Nemours and Company (US)
FEATURES Location/Qualifiers
source 1..4974
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
ORIGIN
Query Match 72.7%; Score 112; DB 6; Length 4974;
Best Local Similarity 100.0%; Pred. No. 5e-12;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGGCCGAGCTGGTCACTCTCGCTCATGTCGAGTCGCGCGGAGCTGTGTCATCTCGCT 60
DB 4863 CGGCCGAGCTGGTCACTCTCGCTCATGTCGAGTCGCGCGGAGCTGTGTCATCTCGCT 4922
QY 61 CATCGTCGAGTCGCGCGCGCGCGGAGTCGAGTCGAGCGAGATGACCACTCC 112
DB 4923 CATCGTCGAGTCGCGCGCGCGCGGAGTCGAGTCGAGCGAGATGACCACTCC 4974
RESULT 6
AX353724/c 4974 bp DNA linear PAT 06-FEB-2002
LOCUS AX353724
DEFINITION Sequence 17 from Patent EP1174510.
ACCESSION AX353724

VERSION AX353724.1 GI:18618779
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Allen,S.M., Butler,K.H., Carlson,T.J. and Ilag,L.L.
TITLE Plasmidial phosphoglucomutase genes
JOURNAL Patent: EP 1174510-A 17 23-JAN-2002;
E.I. du Pont de Nemours and Company (US)
FEATURES Location/Qualifiers
source 1..4974
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
ORIGIN
Query Match 72.7%; Score 112; DB 6; Length 4974;
Best Local Similarity 100.0%; Pred. No. 5e-12;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 43 GGAGCTGGTCACTCTCGCTCATGTCGAGTCGCGCGCGCGGAGCTGACGATGACGAGAT 102
DB 4974 GGAGCTGGTCACTCTCGCTCATGTCGAGTCGCGCGCGCGGAGCTGACGATGACGAGAT 4915
QY 103 GACCAGCTCCGCGCGCGGAGTCGAGTCGAGCGAGATGACCACTCCGCGCG 154
DB 4914 GACCAGCTCCGCGCGCGGAGTCGAGTCGAGCGAGATGACCACTCCGCGCG 4863
RESULT 7
AX392337 6611 bp DNA linear PAT 23-MAR-2002
LOCUS AX392337
DEFINITION Sequence 26 from Patent WO0216565.
ACCESSION AX392337
VERSION AX392337.1 GI:19700690
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE 1
AUTHORS Booth,J.R., Cahoon,R.E., Hiltz,W.D., Kinney,A.J. and Yadav,N.S.
TITLE Nucleotide sequences of a new class of diverged delta-9
JOURNAL stearoyl-acp desaturase genes
Patent: WO 0216565-A 26 28-FEB-2002;
E.I. du Pont de Nemours and Company (US)
FEATURES Location/Qualifiers
source 1..6611
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
/note="Plasmid pBS68"
ORIGIN
Query Match 53.8%; Score 82.8; DB 6; Length 6611;
Best Local Similarity 97.7%; Pred. No. 1.6e-06;
Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 CGGCCGAGCTGGTCACTCTCGCTCATGTCGAGTCGCGCGCGGAGCTGTGTCATCTCGCT 60
DB 5348 CGGCCGAGCTGGTCACTCTCGCTCATGTCGAGTCGCGCGCGGAGCTGTGTCATCTCGCT 5407
QY 61 CATCGTCGAGTCGCGCGCGCGGAGTCGAGTCGAGCGAGATGACCACTCC 86
DB 5408 CATCGTCGAGTCGCGCGCGCGGAGTCGAGTCGAGCGAGATGACCACTCC 5433
RESULT 8
AX392337/c 6611 bp DNA linear PAT 23-MAR-2002
LOCUS AX392337
DEFINITION Sequence 26 from Patent WO0216565.
ACCESSION AX392337
VERSION AX392337.1 GI:19700690

KEYWORDS	unidentified
SOURCE	unidentified
ORGANISM	unclassified.
REFERENCE	1
AUTHORS	Booth,J.R., Cahoon,R.E., Hitz,W.D., Kinney,A.J. and Yadav,N.S.
TITLE	Nucleotide sequences of a new class of diverged delta-9
JOURNAL	stearoyl-acp desaturase genes
FEATURES	Patent: WO 0216565-A 26 28-FEB-2002;
source	E. I. du Pont de Nemours and Company (US)
	Location/Qualifiers
	1..6611
	/organism="unidentified"
	/mol_type="unassigned DNA"
	/db_xref="taxon:32644"
	/note="Plasmid pBS68"
ORIGIN	
Query Match	53.8%; Score 82.8; DB 6; Length 6611;
Best Local Similarity	97.7%; Pred. No.1.6e-06;
Matches	84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY	69 AGTCGCGCGCCGCGCTCGACGATGAGCGAGATGACCACTCCGCGCCGCGACTCGACG 128
Db	5433 ACTCAGCGCGCCGCGCTCGACGATGAGCGAGATGACCACTCCGCGCCGCGACTCGACG 5374
QY	129 ATGAGCGAGATGACCACTCCGCGCG 154
Db	5373 ATGAGCGAGATGACCACTCCGCGCG 5348
RESULT 9	
AX367144	
LOCUS	AX367144 963 bp DNA linear PAT 16-FEB-2002
DEFINITION	Sequence 29 from Patent WO0200904.
ACCESSION	AX367144
VERSION	AX367144.1 GI:18855345
KEYWORDS	
SOURCE	synthetic construct
ORGANISM	synthetic construct
REFERENCE	other sequences; artificial sequences.
AUTHORS	1
TITLE	Glassman,K.F., Gordon-Kamm,W.J., Kinney,A.J., Lowe,K., Steccà,K.L.
JOURNAL	and Nichols,S.E.
FEATURES	Recombinant constructs and their use in reducing gene expression
source	Patent: WO 0200904-A 29 03-JAN-2002;
	E. I. du Pont de Nemours and Company (US) ; PIONEER HI-BRED
	INTERNATIONAL, INC. (US)
	Location/Qualifiers
	1..963
	/organism="synthetic construct"
	/mol_type="unassigned DNA"
	/db_xref="taxon:32630"
	/note="ELVISLIVES complementary region of PKSL149"
ORIGIN	
Query Match	52.6%; Score 81; DB 6; Length 963;
Best Local Similarity	100.0%; Pred. No. 5.1e-06;
Matches	81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	74 GCGGCGCGCGACTCGACGATGAGCGAGATGACCACTCCGCGCCGCGACTCGACGATGAG 133
Db	883 GCGGCGCGCGACTCGACGATGAGCGAGATGACCACTCCGCGCCGCGACTCGACGATGAG 942
QY	134 CGAGATGACCACTCCGCGCG 154
Db	943 CGAGATGACCACTCCGCGCG 963
RESULT 10	
AX367144/c	
LOCUS	AX367144 963 bp DNA linear PAT 16-FEB-2002
DEFINITION	Sequence 29 from Patent WO0200904.

ACCESSION	AX367144
VERSION	AX367144.1 GI:18855345
KEYWORDS	.
SOURCE	synthetic construct
ORGANISM	synthetic construct
REFERENCE	other sequences; artificial sequences.
AUTHORS	1 Glassman,K.F., Gordon-Kamm,W.J., Kinney,A.J., Lowe,K., Stecca,K.L. and Nichols,S.E.
TITLE	Recombinant constructs and their use in reducing gene expression
JOURNAL	Patent: WO 0200904-A 29 03-JAN-2002;
	E.I. du Pont de Nemours and Company (US) ; PIONEER HI-BRED INTERNATIONAL, INC. (US)
FEATURES	Location/Qualifiers
source	1..963
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	/mol_type="unassigned DNA"
	/db_xref="taxon:32630"
	/note="ELVISLIVES complementary region of PKS149"
ORIGIN	
Query Match	52.6%; Score 81; DB 6; Length 963;
Best Local Similarity	100.0%; Pred.No. 5.1e-06;
Matches	81; Conservative 0; Mismatches 0; Indels 0; Gaps 0,
OY	1 CGGCCGAGCTGGTCATCTCGCTCATCTGCAGTCCGCCGCCGAGCTGTCTCCTCGCT 60
Db	963 CGGCCGAGCTGGTCATCTCGCTCATCTGCAGTCCGCCGCCGAGCTGTCTCCTCGCT 904
OY	61 CATCGTCAGTCCGCCGCCG 81
Db	903 CATCGTCAGTCCGCCGCCG 883
RESULT 11	
LOCUS	AX367127 80 bp DNA linear PAT 16-FEB-2002
DEFINITION	Sequence 12 from Patent WO0200904.
ACCESION	AX367127
VERSION	AX367127.1 GI:18855328
KEYWORDS	.
SOURCE	synthetic construct
ORGANISM	synthetic construct
REFERENCE	other sequences; artificial sequences.
AUTHORS	1 Glassman,K.F., Gordon-Kamm,W.J., Kinney,A.J., Lowe,K., Stecca,K.L. and Nichols,S.E.
TITLE	Recombinant constructs and their use in reducing gene expression
JOURNAL	Patent: WO 0200904-A 12 03-JAN-2002;
	E.I. du Pont de Nemours and Company (US) ; PIONEER HI-BRED INTERNATIONAL, INC. (US)
FEATURES	Location/Qualifiers
source	1..80
	/organism="synthetic construct"
	/mol_type="unassigned DNA"
	/db_xref="taxon:32630"
	/note="ELVISLIVES complementary region of PKS106 and PKS124"
ORIGIN	
Query Match	51.9%; Score 80; DB 6; Length 80;
Best Local Similarity	100.0%; Pred.No. 1.3e-05;
Matches	80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	38 CGGCCGAGCTGGTCATCTCGCTCATCTGCAGTCCGCCGCCGACTCGACATGAGC 97
Db	1 CGGCCGAGCTGGTCATCTCGCTCATCTGCAGTCCGCCGCCGACTCGACATGAGC 60
OY	98 GAGATGACCACTCCGCCCG 117
Db	61 GAGATGACCACTCCGCCCG 80

RESULT 12
AX367127/c
LOCUS AX367127 80 bp DNA linear PAT 16-FEB-2002
DEFINITION Sequence 12 from Patent WO0200904.
ACCESSION AX367127
VERSION AX367127.1 GI:18855328
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
E. I. du Pont de Nemours and Company (US) ; PIONEER HI-BRED
INTERNATIONAL, INC. (US)
FEATURES
source
1. 80
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="ELVISLIVES complementary region of PKS106 and
PKS124"

ORIGIN

Query Match 51.9%; Score 80; DB 6; Length 80;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 CGGCCGAGCTGTCATCTCGCTCATCGTCGAGTCGGCGCGCCGCACTCGACGATGAGC 97
|||||
DB 80 CGGCCGAGCTGTCATCTCGCTCATCGTCGAGTCGGCGCGCCGCACTCGACGATGAGC 21

QY 98 GAGATGACCAGCTCCGGCCG 117
|||||
DB 20 GAGATGACCAGCTCCGGCCG 1

RESULT 13
AX392335
LOCUS AX392335 80 bp DNA linear PAT 23-MAR-2002
DEFINITION Sequence 24 from Patent WO0216565.
ACCESSION AX392335
VERSION AX392335.1 GI:19700688
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
E. I. du Pont de Nemours and Company (US)
FEATURES
source
1. 80
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="ELVISLIVES complementary region of PKS106 and
PKS124"

ORIGIN

Query Match 51.9%; Score 80; DB 6; Length 80;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 CGGCCGAGCTGTCATCTCGCTCATCGTCGAGTCGGCGCGCCGCACTCGACGATGAGC 97
|||||
DB 1 CGGCCGAGCTGTCATCTCGCTCATCGTCGAGTCGGCGCGCCGCACTCGACGATGAGC 60

QY 98 GAGATGACCAGCTCCGGCCG 117

DB 61 GAGATGACCAGCTCCGGCCG 80
|||||

RESULT 14
AX392335/c
LOCUS AX392335 80 bp DNA linear PAT 23-MAR-2002
DEFINITION Sequence 24 from Patent WO0216565.
ACCESSION AX392335
VERSION AX392335.1 GI:19700688
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
E. I. du Pont de Nemours and Company (US)
FEATURES
source
1. 80
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="ELVISLIVES complementary region of PKS106 and
PKS124"

ORIGIN

Query Match 51.9%; Score 80; DB 6; Length 80;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 CGGCCGAGCTGTCATCTCGCTCATCGTCGAGTCGGCGCGCCGCACTCGACGATGAGC 97
|||||
DB 80 CGGCCGAGCTGTCATCTCGCTCATCGTCGAGTCGGCGCGCCGCACTCGACGATGAGC 21

QY 98 GAGATGACCAGCTCCGGCCG 117
|||||
DB 20 GAGATGACCAGCTCCGGCCG 1

RESULT 15
AX367129
LOCUS AX367129 92 bp DNA linear PAT 16-FEB-2002
DEFINITION Sequence 14 from Patent WO0200904.
ACCESSION AX367129
VERSION AX367129.1 GI:18855330
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
E. I. du Pont de Nemours and Company (US) ; PIONEER HI-BRED
INTERNATIONAL, INC. (US)
FEATURES
source
1. 92
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="ELVISLIVES PCR primer"

ORIGIN

Query Match 51.9%; Score 80; DB 6; Length 92;
Best Local Similarity 100.0%; Pred. No. 1.2e-05;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 CGGCCGAGCTGTCATCTCGCTCATCGTCGAGTCGGCGCGCCGCACTCGACGATGAGC 97
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Db 7 CGGCCGAGCTGTGTCATCTCGCTCATCTGTCGAGTCGGCGGCCGCCGACTCGACGATGAGC 66
QY 98 GAGATGACCACTCCGCGCC 117
Db 67 GAGATGACCACTCCGCGCC 86

RESULT 16
AX367129/c AX367129 92 bp DNA linear PAT 16-FEB-2002
LOCUS Sequence 14 from Patent WO0200904.
DEFINITION AX367129
ACCESSION AX367129
VERSION AX367129.1 GI:18855330
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS 1 Glassman,K.F., Gordon-Kamm,W.J., Kinney,A.J., Lowe,K., Stecca,K.L. and Nichols,S.E.
TITLE Recombinant constructs and their use in reducing gene expression
JOURNAL Patent: WO 0200904-A 14 03-JAN-2002;
E. I. du Pont de Nemours and Company (US) ; PIONEER HI-BRED INTERNATIONAL, INC. (US)
FEATURES
source location/Qualifiers
1..92
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="ELVISLIVES PCR primer"
ORIGIN

Query Match 51.9%; Score 80; DB 6; Length 92;
Best Local Similarity 100.0%; Pred. No. 1.2e-05;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 38 CGGCCGAGCTGTGTCATCTCGCTCATCTGTCGAGTCGGCGGCCGCCGACTCGACGATGAGC 97
Db 86 CGGCCGAGCTGTGTCATCTCGCTCATCTGTCGAGTCGGCGGCCGCCGACTCGACGATGAGC 27

QY 98 GAGATGACCACTCCGCGCC 117
Db 26 GAGATGACCACTCCGCGCC 7

RESULT 17
AX367139 AX367139 1717 bp DNA linear PAT 16-FEB-2002
LOCUS Sequence 24 from Patent WO0200904.
DEFINITION AX367139
ACCESSION AX367139
VERSION AX367139.1 GI:18855340
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS 1 Glassman,K.F., Gordon-Kamm,W.J., Kinney,A.J., Lowe,K., Stecca,K.L. and Nichols,S.E.
TITLE Recombinant constructs and their use in reducing gene expression
JOURNAL Patent: WO 0200904-A 24 03-JAN-2002;
E. I. du Pont de Nemours and Company (US) ; PIONEER HI-BRED INTERNATIONAL, INC. (US)
FEATURES
source location/Qualifiers
1..1717
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="ELVISLIVES complementary region of pBS68"
ORIGIN

Query Match 29.7%; Score 45.8; DB 6; Length 1717;
Best Local Similarity 95.9%; Pred. No. 21;
Matches 47; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 38 CGGCCGAGCTGTGTCATCTCGCTCATCTGTCGAGTCGGCGGCCGCCGACT 86
Db 1 CGGCCGAGCTGTGTCATCTCGCTCATCTGTCGAGTCGGCGGCCCGCTGAGT 49

RESULT 18
AX367139/c AX367139 1717 bp DNA linear PAT 16-FEB-2002
LOCUS Sequence 24 from Patent WO0200904.
DEFINITION AX367139
ACCESSION AX367139
VERSION AX367139.1 GI:18855340
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS 1 Glassman,K.F., Gordon-Kamm,W.J., Kinney,A.J., Lowe,K., Stecca,K.L. and Nichols,S.E.
TITLE Recombinant constructs and their use in reducing gene expression
JOURNAL Patent: WO 0200904-A 24 03-JAN-2002;
E. I. du Pont de Nemours and Company (US) ; PIONEER HI-BRED INTERNATIONAL, INC. (US)
FEATURES
source location/Qualifiers
1..1717
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="ELVISLIVES complementary region of pBS68"
ORIGIN

Query Match 29.7%; Score 45.8; DB 6; Length 1717;
Best Local Similarity 95.9%; Pred. No. 21;
Matches 47; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 69 AGTCGGCGGCCCGCGACTCGACGATGAGCGAGATGACCACTCCGCGCC 117
Db 49 ACTCAGCGGCCCGCGACTCGACGATGAGCGAGATGACCACTCCGCGCC 1

RESULT 19
STES79650 STES79650 13802 bp. RNA linear BCT 17-MAR-2004
LOCUS Strain ATCC 17920.
DEFINITION
ACCESSION
VERSION AJ579650.1 GI:45544448
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS 1 Kharel,M.K., Basnet,D.B., Lee,H.C., Liou,K., Woo,J.S., Kim,B.G. and Sohng,J.K.
TITLE Isolation and characterization of the tobramycin biosynthetic gene cluster from Streptomyces tenebrarius
JOURNAL FEMS Microbiol. Lett. 230 (2), 185-190 (2004)
PUBMED 14757238
REFERENCE
AUTHORS 2 Kharel,M.K., Lee,H.C., Liou,K., Woo,J.S. and Sohng,J.K.
TITLE An approach for cloning biosynthetic genes of 2-deoxystreptamine containing aminocyclitol antibiotics: isolation of biosynthetic gene cluster of tobramycin from S. tenebrarius
JOURNAL Unpublished
REFERENCE
AUTHORS 3 (bases 1 to 13802)
TITLE Direct Submission
JOURNAL Submitted (01-AUG-2003) Sohng J.K., Chemistry, Sun Moon University, 100 Kalsanri, Tangjeongmyun, Asan si, Chungchungnamdo, 336-708,

SOUTH KOREA
location/Qualifiers
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/organism="Streptomyces tenebrarius"
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/strain="ATCC 17920"
/isolation_source="soil"
/db_xref="taxon:1933"
/country="Mexico"
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/protein_id="CAE22469.1"
/db_xref="GI:45544449"
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KARTEMDDAALDPRRVHRLAYLASDRFAEGDTEERTEIRRRFGLDGQPVLYVGR
IAAKGVFEFVEAAAEARRRGRNCRFLVAGDGPTRQIEKLAEDRGVADRITITGFLP
HELIPSVMALSQVLVPSRYBELGIVILECMSMRPIVAHDVNGVHKLIEHGRGTLV
PPDTPAMADAIERALDDBELRERIAETAAPLPSAKYSLTTAADQLTDIYRELGCV"
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/db_xref="GI:45544450"
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VLDDGCHAVEICRWLGGAEVRAVTARSQVRPRAGVEDQATLLERADGALGQCD
VSWACPGEEITTEVLGTSRAGADLMAGVHAFSERGASVMEPQGWPRMEWV
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/evidence=experimental
/transl_table=11
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/protein_id="CAE22471.1"
/db_xref="GI:45544451"
/translation="MQTTITMGDVQYPYRLGTCVDGIVTRLGELEASHYLVLCDAT
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VEVLADTAMIGTLPVREIRSGLCEVVKNALIRPSMIDFLAELRPGRVADVDLRMM
IDESVAAKAQVTEHDKYERREGVLEYGHTVGHALLEHSHGAVSHGAGVGMVAAAE
VARLGHVDADLVEILHRELVGKVAATTLPAVDYTEIYRLGFDNKGYPPLADHY
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/product="putative 2-deoxy-scyll-o-inosose
aminotransferase"
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/db_xref="GI:45544452"
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GPYRGIESAERRFARDFAYNGVAHCVPAAGTASIMLALBESCGVGDEVIAFGLSW
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AVADRHGLPLIEDCAQAHGAEHGRKVGSGVDYGTFSMQHSKFLTSGECAAITNSAE
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CDS
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/protein_id="CAE22473.1"
/db_xref="GI:45544453"
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VPGAMSLGFFYEHVSEYTGLDGDNPGKLMGLAAHGTVDETLSAFAPDSDGRLNLID
PQARDPEDWDEYSTERAWFAHLERIYRLPNEFVRRYDPAKGRVVRTDRDPYERD
LAATAQALERAVERGLADSVLARTGERTLFVAGVGLNATMNGKLLTRSTVDKMFVP
VASDIGVSLGAANAVALGDRIPMGDTAAWGPFSPOQVRALDRGTGLAYREPANL
EREVAALIASGKVVGAQGRGEVGPRLAGORSLGSAHSPTRKHINLRVKDREWRP
FAPSMLSVSDOVLEVDADFPYIMTTKVRAAYAERLPSVHEBWSTRPQVTEASNP
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GGPIPGADVEDHEDPDGMAFARRHGRWTRDGPMTAMALGGTYFYAGMSYRQDS
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PTPGLALAEGARALNLTPLPTPAISGIRDRFGPGAQATPCTSPSCPTGAKADV
RVLAPAEGDVSVLVHTRVDRLVAGSGSHRDVAEVDGRTGTRTLRARFLVAANAIO
SALLLRSTSRLEPDGLNGNGLVGRHLAMKNSVYVRGVPRRLPGYTPLRHRYSSVC
VLDTLTGEEFPDVGGLIHEANPWEPAEREARGTVLOVECLDGRPOARNRVLSR
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/db_xref="GI:45544455"
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LAERLDMFPMAQALFYRTGSCAVSVARLSQHTGRTAVLTSGYGHMDHMLEAVP
EAKLFPYSYATEFHDLDVRYALDRHADEIAAVVTPPTPHPLSEHYRTLRLDLAEAG
CLFVLDEVKTKMRAGKGLSARAGLEPAVTVSKGLANGHSISAVVSGSRITTEGLAEA
HWMSTYQNEQVGYAAALSTDVFLREDAVVERTGRTVERAFPSAERGLPVEVHG
WGPMPDLDFSAEEDLPERQLALLRHGVFCDVGDDEFNLMYRMADHLDELLERTAAI
ASV"
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AAMGSGRAVSLSTLTAITLAIAGLFGYPAVGAVSGSLGSLACALALSFSEPRE
QVDESGGWRWYATFRAGVSEVRGDRVLRVAVLAASLHMTAIDEYFPMLARANGA
STMPVPLVAVTVCAAVGSGLVGRTHAPSGALGIALIASAALLAAGALSGLQSGML
AVGVSFGLVQWALVLADTRLQDAITGPARATVTSVVGFSGEVASVGFYLAAGAVSTVT
SMSTLVAMFAVPLVLIAVAFRWLRREPCPTGQVRPEPEPRRD"
complement(11379. .12398)
gene

Query Match	Best Local Similarity	Score	DB 1	Length
Matches 90; Conservative	58.8%;	Pred. No. 83;	Mismatches 62;	Indels 1; Gaps 1;
QY	2	GGCCGAGCTGTCATCTCGCTCATCTCGAGTCGCGCGCCGAGCTGTCATCTCGCTC	61	
Db	2666	GGCAGCGGCTGTAGTACCCCGCTGTGTTCGAAGCCGAGCCGCTGATCTCCTCGCTC	2725	
QY	62	ATCGTCGAGTCGCGCGCCGCGCACTCGACGATGAGCGAGATGACCACTCCGCGCCGCA	121	
Db	2726	GGCAGCTCGCGCGCGAGCGCTGTCGCGAGCCGACCTTGCCGACCACTCCTGTGAG	2784	
QY	122	CTCGACGATGAGCGAGATGACCACTCCGCGCCG 154		
Db	2785	CTCGACGAGTTCGCGCTGCGCTGCGCGCGCG 2817		
RESULT 20	STB579650/c			
LOCUS	STB579650	13802 bp	RNA	linear
DEFINITION	Streptomyces tenebrarius tobramycin biosynthetic gene cluster,			
ACCESSION	AJ579650			
VERSION	AJ579650.1	GI:45544448		
KEYWORDS	2-deoxy-scyllo-inosose aminotransferase; 2-deoxy-scyllo-inosose synthase; carbamoyltransferase; dehydrogenase; glycosyltransferase; ORF1; ORF2; ORF3; tacA gene; tacD gene; tbmA gene; tbmB gene; tbmC gene; tbmD gene; tbmE gene; transport protein.			
SOURCE	Streptomyces tenebrarius			
ORGANISM	Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.			
REFERENCE	1	Kharel, M.K., Basnet, D.B., Lee, H.C., Liou, K., Woo, J.S., Kim, B.G. and Sohn, J.K.		
AUTHORS				
TITLE	Isolation and characterization of the tobramycin biosynthetic gene cluster from Streptomyces tenebrarius			
JOURNAL	FEMS Microbiol. Lett. 230 (2), 185-190 (2004)			
PUBMED	14757238			
REFERENCE	2	Kharel, M.K., Lee, H.C., Liou, K., Woo, J.S. and Sohn, J.K.		
AUTHORS				
TITLE	An approach for cloning biosynthetic genes of 2-deoxystreptamine containing aminocyclitol antibiotics: isolation of biosynthetic gene cluster of tobramycin from S. tenebrarius			
JOURNAL	Unpublished			
REFERENCE	3	(bases 1 to 13802)		
AUTHORS	Sohn, J.K.			
TITLE	Direct Submission			
JOURNAL	Submitted (01-AUG-2003)			
	Sohn, J.K., Chemistry, Sun Moon University,			

100 Kalsanri, Tangjeongmyun, Asan si, Chungchungnamdo, 336-708,
SOUTH KOREA

Location/Qualifiers

1. .13802

/organism="Streptomyces tenebrarius"

/mol_type="genomic RNA"

/strain="ATCC 17920"

/isolation_source="soil"

/db_xref="taxon:1933"

/country="Mexico"

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/gene="tbmd"

complement(1. .1176)

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/product="putative glycosyltransferase"

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/db_xref="GI:45544449"

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KARTEMDDAALDPRVRHRLAYLASDRFAEGDTEERTETRRRFGLDTGQPVLYGR
IAEKGEFFVEAAAEIARRGNCRFLVAGDPTROEIKLADRGVADRITITGFLP
HELIPSMALSQVLVPSRYEELGIVILECMSMRPIVAHDVNGVHKLIEHRTGLLV
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complement(1280. .2323)

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/product="putative dehydrogenase"

/protein_id="CAE22470.1"

/db_xref="GI:45544450"

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GLVLAHGSNFVHSPKFRVRRELVDADAFGRPHLARVVYVNGGPDGCLDPALAGG
VLLDIGCHAVEICRWLGGAEVRAVTARSQVRPRAGRVEDQATLLLEFADGALGQC
VSWACPGGEITTEVLTSGRAGADLMAGMGVHAFSEGFASVWEPNQGWRPEWEW
RASGYTHQDHAVEAVLDGTPPLHSAVEAWTSARVLEAAESAATGRTVELAPSPNGH
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complement(2494. .3654)

/gene="tbmA"

complement(2494. .3654)

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/evidence=experimental

/transl_table=11

/product="2-deoxy-scyllo-inosose synthase"

/protein_id="CAE22471.1"

/db_xref="GI:45544451"

/translation="MOTTTITMGDVQPYRLGTGCVDIGIVTRLGELASHLYLGDAT
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GGGVTGNIAGLLAALFRGIRLVHPPTTVAMDSVLSKQAVNAOVGKNLVGTFYEP
VEVLADTAMLGTLPYREIRSGLCEVKNALAIRSMIDFLAELRPDGRYADIVLRWM
IDESVAAKAQVTEHDKYEREGVLBYGHTVGHALHSHAGAVSHGAGVGVAAAE
VARRLGHVDADLVELHRELVGKGVATTLPADVPEETIYRLGFDNKRGYQPLPADHY
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complement(3684. .4958)

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complement(3684. .4958)

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/product="putative 2-deoxy-scyllo-inosose
aminotransferase"

/protein_id="CAE22472.1"

/db_xref="GI:45544452"

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VASASTIVGNAVFLVDIDRITCLDPAVAEAITPATKAVVVLHYSAAVIDALR
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CDS	12867. .13802 /note="ORF3" /codon_start=1 /transl_table=11 /product="hypothetical protein" /protein_id="CAE22478.1" /db_xref="GI:45544458" /translation="MTTHAVDTKIRPLKESHPHRAAGTRREAAHFLSLPGAS"
Query Match	27.1%; Score 41.8; DB 1; Length 13802;
Best Local Similarity	58.8%; Pred. No. 83;
Matches	90; Conservative 0; Mismatches 62; Indels 1; Gaps 1;
Qy	1 CGGCCGAGCTGTCATCTCGCTCATCTCGAGTCGGCGCGGAGCTGTCATCTCGCT 60
Db	2817 CGGCTCGGAGCAGTCGACGCCGACCTCTGTCAG-CTGCACAGGAGCTGTGCGAAGT 2759
Qy	61 CATCGTCAGTCGGCGCGCGCGCTCGACATGACGAGATGACGAGATGACCGCGCGCG 120
Db	2758 CGGCTCGGAGCAGCAGCTGCCGCGCGACGTCGCCGACGAGAGATCACCTACCGGCTCGG 2699
Qy	121 ACTCGACATGACGAGATGACCGAGCTCGCGCC 153
Db	2698 CTTGACACACAGCGGGGCTACCAAGCCGCTGCC 2666

RESULT 21
BX571966_08

WPCOMMENT

Sequence split into 32 fragments LOCUS BX571966 Accession BX571966

Fragment Name	Begin	End
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BX571966_01	100001	210000
BX571966_02	200001	310000
BX571966_03	300001	410000
BX571966_04	400001	510000
BX571966_05	500001	610000
BX571966_06	600001	710000
BX571966_07	700001	810000
BX571966_08	800001	910000
BX571966_09	900001	1010000
BX571966_10	1000001	1110000
BX571966_11	1100001	1210000
BX571966_12	1200001	1310000
BX571966_13	1300001	1410000
BX571966_14	1400001	1510000
BX571966_15	1500001	1610000
BX571966_16	1600001	1710000
BX571966_17	1700001	1810000
BX571966_18	1800001	1910000
BX571966_19	1900001	2010000
BX571966_20	2000001	2110000
BX571966_21	2100001	2210000
BX571966_22	2200001	2310000
BX571966_23	2300001	2410000
BX571966_24	2400001	2510000
BX571966_25	2500001	2610000

BX571966_26 2600001 2710000
BX571966_27 2700001 2810000
BX571966_28 2800001 2910000
BX571966_29 2900001 3010000
BX571966_30 3000001 3110000
BX571966_31 3100001 3173005
Continuation (9 of 32) of BX571966 from base 800001 (BX571966 Burkholderia pseudomallei)

Query Match 25.1%; Score 38.6; DB 1; Length 110000;
Best Local Similarity 59.6%; Pred. No. 2.2e+02;
Matches 65; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY 3 GCCGAGCTGTCATCTCGCTCATCTCGAGTCGGCGCCGAGCTGTCATCTCGCTCA 62
Db 31704 GGCCGAGCCGATCGCGCAGCTCGTACAGCTCGCGGAGCGGACGCCCTCGTCGAGACGA 31763

QY 63 TCCTCGAGTCGGCGCGCCGCGACTCGACGATGAGCGAGATGACCACTC 111
Db 31764 TCGCCGCGCTGCGCTCGCGCTGCTCGACGATCAGCGGATGGCTGCTC 31812

RESULT 22
BX571966_08/c
WPCOMMENT
Sequence split into 32 fragments LOCUS BX571966 Accession BX571966

Fragment Name	Begin	End
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BX571966_01	100001	210000
BX571966_02	200001	310000
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BX571966_31	3100001	3173005

Continuation (9 of 32) of BX571966 from base 800001 (BX571966 Burkholderia pseudomallei)

Query Match 25.1%; Score 38.6; DB 1; Length 110000;
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QY 104 ACCAGCTCGGCGCCGCGACTCGACGATGAGCGAGATGACCACTCCGCGC 152
Db 31752 ACGGCGTCGCTCGCGGAGCTGTACGAGCTGCGGATCGGCTCGGCC 31704

RESULT 23
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LOCUS
DEFINITION
Pseudomonas aeruginosa PA01, section 407 of 529 of the complete genome.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Pseudomonas aeruginosa PA01
Pseudomonas aeruginosa PA01
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas.

REFERENCE
AUTHORS
1 (bases 1 to 10348)
Stover, C.K., Pham, X.-Q.T., Erwin, A.L., Mizoguchi, S.D., Warrenner, P., Hickey, M.J., Brinkman, F.S.L., Huftagle, W.O., Kowalik, D.J., Lagrou, M., Garber, R.L., Goltry, L., Tolentino, E., Westbrock-Wadman, S., Yuan, Y., Brody, L.L., Coulter, S.N., Folger, K.R., Kas, A., Larbig, K., Lim, R.M., Smith, K.A., Spencer, D.H., Wong, G.K.-S., Wu, Z. and Paulsen, I.T.

TITLE
Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen

JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
2 (bases 1 to 10348)
10984043
Stover, C.K., Pham, X.-Q.T., Erwin, A.L., Mizoguchi, S.D., Warrenner, P., Hickey, M.J., Brinkman, F.S.L., Huftagle, W.O., Kowalik, D.J., Lagrou, M., Garber, R.L., Goltry, L., Tolentino, E., Westbrock-Wadman, S., Yuan, Y., Brody, L.L., Coulter, S.N., Folger, K.R., Kas, A., Larbig, K., Lim, R.M., Smith, K.A., Spencer, D.H., Wong, G.K.-S., Wu, Z., Paulsen, I.T., Reizer, J., Sater, M.H., Hancock, R.E.W., Lory, S. and Olson, M.V.

TITLE
JOURNAL
Submitted (16-MAY-2000) Department of Medicine and Genetics, University of Washington Genome Center, University Of Washington, Box 352145, Seattle, WA 98195, USA

REFERENCE
AUTHORS
CONSRTM
JOURNAL
Submitted (04-FEB-2003) Department of Molecular Biology and Biochemistry, Simon Fraser University, 8888 University Dr., Burnaby, British Columbia V5A 1S6, Canada

COMMENT

This represents the February 3, 2003 version of the continually updated, reviewed, Pseudomonas aeruginosa PA01 genome annotation, from PseudocAP (see <http://www.pseudomonas.com> for latest updates and links to alternate annotations). PseudocAP is coordinated by Fiona S.L. Brinkman (Simon Fraser University, Canada) and Robert E.W. Hancock (University of British Columbia, Canada). We welcome submission through www.pseudomonas.com of any proposed changes.

'Protein name confidence' is used to rate our confidence of the accuracy of the protein name.

Class 1: Function experimentally demonstrated in P. aeruginosa.

Class 2: Function of highly similar gene experimentally demonstrated in another organism (and gene context consistent in terms of pathways its involved in, if known).

Class 3: Function proposed based on presence of conserved amino acid motif, structural feature or limited sequence similarity to an experimentally studied gene.

Class 4: Homologs of previously reported genes of unknown function, or no similarity to any previously reported sequences.

FEATURES
Location/Qualifiers

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Db 8072 AGCGGCTGACCAAGTCCGGGGTGAAGATCATCAGCAGC 8110
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LOCUS AE004846 10348 bp DNA linear BCF 19-FEB-2003

DEFINITION Pseudomonas aeruginosa PA01, section 407 of 529 of the complete genome.
ACCESSION AE004846 AE004091
VERSION AE004846.1 GI:9950517
KEYWORDS
SOURCE
ORGANISM Pseudomonas aeruginosa PA01
Pseudomonas aeruginosa PA01
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas.
REFERENCE 1 (bases 1 to 10348)
AUTHORS Stover,C.K., Pham,X.-Q.T., Erwin,A.L., Mizoguchi,S.D., Warrenner,P., Hickey,M.J., Brinkman,F.S.L., Hufnagle,W.O., Kowalik,D.J., Lagrou,M., Garber,R.L., Goltry,L., Tolentino,E., Westbrock-Wadman,S., Yuan,Y., Brody,L.L., Coulter,S.N., Folger,K.R., Kas,A., Larbig,K., Lim,R.M., Smith,K.A., Spencer,D.H., Wong,G.K.-S., Wu,Z. and Paulsen,I.T.
TITLE Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen
JOURNAL Nature 406 (6799), 959-964 (2000)
MEDLINE 20437337
PUBMED 10984043
REFERENCE 2 (bases 1 to 10348)
AUTHORS Stover,C.K., Pham,X.-Q.T., Erwin,A.L., Mizoguchi,S.D., Warrenner,P., Hickey,M.J., Brinkman,F.S.L., Hufnagle,W.O., Kowalik,D.J., Lagrou,M., Garber,R.L., Goltry,L., Tolentino,E., Westbrock-Wadman,S., Yuan,Y., Brody,L.L., Coulter,S.N., Folger,K.R., Kas,A., Larbig,K., Lim,R.M., Smith,K.A., Spencer,D.H., Wong,G.K.-S., Wu,Z., Paulsen,I.T., Reizer,J., Sater,M.H., Hancock,R.E.W., Lory,S. and Olson,M.V.
TITLE Direct Submission
JOURNAL Submitted (16-MAY-2000) Department of Medicine and Genetics, University of Washington Genome Center, University Of Washington, Box 352145, Seattle, WA 98195, USA
REFERENCE 3 (bases 1 to 10348)
AUTHORS Pseudomonas aeruginosa Community Annotation Project (PseudocAP)
CONSRM Direct Submission
TITLE Submitted (04-FEB-2003) Department of Molecular Biology and Biochemistry, Simon Fraser University, 8888 University Dr., Burnaby, British Columbia V5A 1S6, Canada
JOURNAL
COMMENT
This represents the February 3, 2003 version of the continually updated, reviewed, Pseudomonas aeruginosa PA01 genome annotation, from PseudocAP (see http://www.pseudomonas.com for latest updates and links to alternate annotations). PseudocAP is coordinated by Fiona S.L. Brinkman (Simon Fraser University, Canada) and Robert E.W. Hancock (University of British Columbia, Canada). We welcome submission through www.pseudomonas.com of any proposed changes.
'Protein name confidence' is used to rate our confidence of the accuracy of the protein name.
Class 1: Function experimentally demonstrated in P. aeruginosa.
Class 2: Function of highly similar gene experimentally demonstrated in another organism (and gene context consistent in terms of pathways its involved in, if known).
Class 3: Function proposed based on presence of conserved amino acid motif, structural feature or limited sequence similarity to an experimentally studied gene.
Class 4: Homologs of previously reported genes of unknown function, or no similarity to any previously reported sequences.

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KEYWORDS
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ORGANISM     Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
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REFERENCE    1
AUTHORS      Omura,S., Ikeda,H., Ishikawa,J., Hanamoto,A., Takahashi,C.,
              Shinose,M., Takahashi,Y., Horikawa,H., Nakazawa,H., Osonoe,T.,
              Kikuchi,H., Shiba,T., Sakaki,Y. and Hattori,M.
TITLE        Genome sequence of an industrial microorganism Streptomyces
              avermitilis: deducing the ability of producing secondary
              metabolites
              Proc. Natl. Acad. Sci. U.S.A. 98 (21), 12215-12220 (2001)
JOURNAL      21477403
MEDLINE      11572948
PUBMED
REFERENCE    2
AUTHORS      Ikeda,H., Ishikawa,J., Hanamoto,A., Shinose,M., Kikuchi,H.,
              Shiba,T., Sakaki,Y., Hattori,M. and Omura,S.
TITLE        Complete genome sequence and comparative analysis of the industrial
              microorganism Streptomyces avermitilis
              Nat. Biotechnol. 21 (5), 526-531 (2003)
JOURNAL      22608306
MEDLINE      12692562
PUBMED
REFERENCE    3 (bases 1 to 301925)
AUTHORS      Omura,S., Ikeda,H., Ishikawa,J., Hanamoto,A., Takahashi,C.,
              Shinose,M., Takahashi,Y., Horikawa,H., Nakazawa,H., Osonoe,T.,
              Kushida,N., Director-General of Biotechnology Center, Shiba,T.,
              Sakaki,Y. and Hattori,M.
TITLE        Direct Submission
JOURNAL      Submitted (29-MAR-2002) Director-General of Biotechnology Center,
              National Institute of Technology and Evaluation, Biotechnology
              Center; 2-49-10 Nishihara, Shibuya-ku, Tokyo 151-0066, Japan
              (E-mail:bio@nite.go.jp, URL:http://www.bio.nite.go.jp/,
              Tel:81-3-3481-1933, Fax:81-3-3481-8424)
COMMENT      This work was done in collaboration with Haruo Ikeda(*1), Jun
              Ishikawa(*2), Akiharu Hanamoto(*3), Chigusa Takahashi(*3), Mayumi
              Shinose(*3), Hiroshi Horikawa(*4), Hidekazu Nakazawa(*4), Tomomi
              Osonoe(*4), Norihiro Kushida(*4), Hisashi Kikuchi(*4), Tadayoshi
              Shiba(*5), Yoshiyuki Sakaki(*6,*7), Masahira Hattori(*1,*7)
              and Satoshi Omura(*1,*3).
              Final finishing process and all annotation were done by H. Ikeda
              and J. Ishikawa.
              *1 Kitasato Institute for Life Sciences, Kitasato University
              *2 National Institute of Infectious Diseases
              *3 The Kitasato Institute
              *4 National Institute of Technology and Evaluation
              *5 School of Science, Kitasato University
              *6 Institute of Medical Science, University of Tokyo
              *7 RIKEN, Genomic Sciences Center
              Following url is also available.
              http://avermitilis.ls.kitasato-u.ac.jp.
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SOURCE
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CDS
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DEFINITION			
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VERSION			
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SOURCE			
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AP005046 BA000030			
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Streptomyces avermitilis MA-4680			
24.7%; Score 38; DB 1; Length 301925;			
Best Local Similarity 59.1%; Pred. No. 2.4e+02;			
Matches 65; Conservative 0; Mismatches 45; Indels 0; Gaps 0;			

ORGANISM	Streptomyces avermitilis MA-4680
REFERENCE	Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
AUTHORS	1 Omura, S., Ikeda, H., Ishikawa, J., Hanamoto, A., Takahashi, C., Shinose, M., Takahashi, Y., Horikawa, H., Nakazawa, H., Osone, T., Kikuchi, H., Shiba, T., Sakaki, Y. and Hattori, M.
TITLE	Genome sequence of an industrial microorganism Streptomyces avermitilis: deducing the ability of producing secondary metabolites
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 98 (21), 12215-12220 (2001)
MEDLINE	21477403
PUBMED	11572948
REFERENCE	2
AUTHORS	Ikeda, H., Ishikawa, J., Hanamoto, A., Shinose, M., Kikuchi, H., Shiba, T., Sakaki, Y., Hattori, M. and Omura, S.
TITLE	Complete genome sequence and comparative analysis of the industrial microorganism Streptomyces avermitilis
JOURNAL	Nat. Biotechnol. 21 (5), 526-531 (2003)
MEDLINE	22608306
PUBMED	12692562
REFERENCE	3 (bases 1 to 301925)
AUTHORS	Omura, S., Ikeda, H., Ishikawa, J., Hanamoto, A., Takahashi, C., Shinose, M., Takahashi, Y., Horikawa, H., Nakazawa, H., Osone, T., Kushida, N., Director-General of Biotechnology Center, Shiba, T., Sakaki, Y. and Hattori, M.
TITLE	Direct Submission
JOURNAL	Submitted (29-MAR-2002) Director-General of Biotechnology Center, National Institute of Technology and Evaluation, Biotechnology Center; 2-49-10 Nishihara, Shibuya-ku, Tokyo 151-0066, Japan (E-mail:bioelite.go.jp, URL:http://www.bio.nite.go.jp/, Tel:81-3-3481-1933, Fax:81-3-3481-8424)
COMMENT	This work was done in collaboration with Haruo Ikeda(*1), Jun Ishikawa(*2), Akiharu Hanamoto(*3), Chigusa Takahashi(*3), Mayumi Shinose(*3), Hiroshi Horikawa(*4), Hidekazu Nakazawa(*4), Tomomi Osone(*4), Norihiro Kushida(*4), Hisashi Kikuchi(*4), Tadayoshi Shiba(*5), Yoshiyuki Sakaki(*6,*7), Masahira Hattori(*1,*7) and Satoshi Omura(*1,*3). Final finishing process and all annotation were done by H. Ikeda and J. Ishikawa.
FEATURES	*1 Kitasato Institute for Life Sciences, Kitasato University *2 National Institute of Infectious Diseases *3 The Kitasato Institute *4 National Institute of Technology and Evaluation *5 School of Science, Kitasato University *6 Institute of Medical Science, University of Tokyo *7 RIKEN, Genomic Sciences Center Following url is also available. http://avermitilis.is.kitasato-u.ac.jp.
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Query Match 24.7%; Score 38; DB 1; Length 301925;
Best Local Similarity 59.1%; Pred. No. 2.4e+02;
Matches 65; Conservative 0; Mismatches 45; Indels 0; Gaps 0;
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RESULT 27
AC134925 148829 bp DNA linear PLN 21-MAR-2004
LOCUS AC134925
DEFINITION Oryza sativa (japonica cultivar-group) chromosome 11 clone
OSJNBa0041J17, complete sequence.
ACCESSION AC134925
VERSION AC134925.4 GI:45598398
KEYWORDS HTG.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

REFERENCE
AUTHORS
1 (bases 1 to 148829)
Ghazi,I.A., Yadav,M., Dixit,R., Singh,A., Srivastava,S.K.,
Pal,A.K., Dalal,V., Batra,K., McCombie,W.R., *Spiegel,L., *de la
Bastide,M., *Zutavern,T., *Muller,S., *Nascimento,L., *Baliya,V.,
*Bell,M., *Miller,B., *Katzenberger,F., *Andrade,M.V., *Dike,S.,
*O'Shaughnessy,A., *Palmer,L., Gaikwad,K., Sharma,T.R.,
Mohapatra,T. and Singh,N.K.
Oryza sativa (japonica cultivar-group) chromosome 11 BAC clone
OSJNBa0041J17, complete sequence
Unpublished
*Lita Annenberg Hazen Genome Center, Cold Spring Harbor Laboratory,
1 Bungtown Road, Cold Spring Harbor, NY 11724, USA.
2 (bases 1 to 148829)
Ghazi,I.A., Yadav,M., Bhargava,A., Dixit,A., Swain,S.C., Batra,K.,
Singh,A., Pal,S., Sureshbabu,K., Srivastava,S., Pal,A.K., Dalal,V.,
Gaikwad,K., Sharma,T.R., Mohapatra,T. and Singh,N.K.
Direct Submission
Submitted (02-OCT-2002) IIRGS, NRC on Plant Biotechnology, Indian
Agricultural Research Institute, LBS Centre, New Delhi, Delhi
110012, India
3 (bases 1 to 148829)
Ghazi,I.A., Yadav,M., Bhargava,A., Dixit,A., Swain,S.C., Batra,K.,
Singh,A., Pal,S., Sureshbabu,K., Srivastava,S., Pal,A.K., Dalal,V.,
Gaikwad,K., Sharma,T.R., Mohapatra,T. and Singh,N.K.
Direct Submission
Submitted (28-FEB-2003) IIRGS, NRC on Plant Biotechnology, Indian
Agricultural Research Institute, LBS Centre, New Delhi, Delhi
110012, India
4 (bases 1 to 148829)
Ghazi,I.A., Yadav,M., Dixit,R., Singh,A., Srivastava,S.K.,
Pal,A.K., Dalal,V., Batra,K., McCombie,W.R., Spiegel,L., de la
Bastide,M., Zutavern,T., Muller,S., Nascimento,L., Baliya,V.,
Bell,M., Miller,B., Katzenberger,F., Andrade,M.V., Dike,S.,
O'Shaughnessy,A., Palmer,L., Gaikwad,K., Sharma,T.R., Mohapatra,T.
and Singh,N.K.
Direct Submission
Submitted (21-MAR-2004) IIRGS, NRC on Plant Biotechnology, Indian
Agricultural Research Institute, LBS Centre, New Delhi, Delhi
110012, India
COMMENT
On Mar 21, 2004 this sequence version replaced gi:28604232.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. This BAC clone was
sequenced to phase II by the National Research Centre on Plant
Biotechnology, Indian Agricultural Research Institute, New Delhi
and was completed to phase III by the Cold Spring Harbor Laboratory
Genome Center under the Indo-US collaboration. Clone OSJNBa0041J17
overlaps clone OSJNBa0007D07 from base 100381 to base 148829. The
overlap is from base 1 to base 48448 on OSJNBa0007D07.
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LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE
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OSJNBa0041J17, complete sequence.	chromosome 11 clone				
AC134925					
AC134925.4	GI:45598398				
HTG.					
Oryza sativa (japonica cultivar-group)					

ORGANISM	Oryza sativa (japonica cultivar-group) Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartioideae; Oryzeae; Oryza.
REFERENCE AUTHORS	1 (bases 1 to 148829) Ghazi,I.A., Yadav,M., Dixit,R., Singh,A., Srivastava,S.K., Pal,A.K., Dalal,V., Batra,K., *McCombie,W.R., *Spiegel,L., *de la Bastide,M., *Zutavern,T., *Muller,S., *Nascimento,L., *Balija,V., *Bell,M., *Miller,B., *Katzenberger,F., *Andrade,M.V., *Dike,S., *O'Shaughnessy,A., *Palmer,L., Gaikwad,K., Sharma,T.R., Mohapatra,T. and Singh,N.K. Oryza sativa [japonica cultivar-group] chromosome 11 BAC clone OSJNBa004IJ17, complete sequence
JOURNAL REMARK	Unpublished *Lita Annenberg Hazen Genome Center, Cold Spring Harbor Laboratory, 1 Bungtown Road, Cold Spring Harbor, NY 11724, USA.
REFERENCE AUTHORS	2 (bases 1 to 148829) Ghazi,I.A., Yadav,M., Bhargava,A., Dixit,A., Swain,S.C., Batra,K., Singh,A., Pal,S., Sureshabu,K., Srivastava,S., Pal,A.K., Dalal,V., Gaikwad,K., Sharma,T.R., Mohapatra,T. and Singh,N.K. Direct Submission
TITLE JOURNAL	Submitted (02-OCT-2002) IIRGS, NRC on Plant Biotechnology, Indian Agricultural Research Institute, LBS Centre, New Delhi, Delhi 110012, India
REFERENCE AUTHORS	3 (bases 1 to 148829) Ghazi,I.A., Yadav,M., Bhargava,A., Dixit,A., Swain,S.C., Batra,K., Singh,A., Pal,S., Sureshabu,K., Srivastava,S., Pal,A.K., Dalal,V., Gaikwad,K., Sharma,T.R., Mohapatra,T. and Singh,N.K. Direct Submission
TITLE JOURNAL	Submitted (28-FEB-2003) IIRGS, NRC on Plant Biotechnology, Indian Agricultural Research Institute, LBS Centre, New Delhi, Delhi 110012, India
REFERENCE AUTHORS	4 (bases 1 to 148829) Ghazi,I.A., Yadav,M., Dixit,R., Singh,A., Srivastava,S.K., Pal,A.K., Dalal,V., Batra,K., McCombie,W.R., Spiegel,L., de la Bastide,M., Zutavern,T., Muller,S., Nascimento,L., Balija,V., Bell,M., Miller,B., Katzenberger,F., Andrade,M.V., Dike,S., O'Shaughnessy,A., Palmer,L., Gaikwad,K., Sharma,T.R., Mohapatra,T. and Singh,N.K. Direct Submission
TITLE JOURNAL	Submitted (21-MAR-2004) IIRGS, NRC on Plant Biotechnology, Indian Agricultural Research Institute, LBS Centre, New Delhi, Delhi 110012, India
COMMENT	On Mar 21, 2004 this sequence version replaced gi:28604232. This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. This BAC clone was sequenced to phase II by the National Research Centre on Plant Biotechnology, Indian Agricultural Research Institute, New Delhi and was completed to phase III by the Cold Spring Harbor Laboratory Genome Center under the Indo-US collaboration. Clone OSJNBa004IJ17 overlaps clone OSJNBa0007D07 from base 100381 to base 148829. The overlap is from base 1 to base 48448 on OSJNBa0007D07.
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misc_feature	
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Best Local Similarity 53.0%; Pred. No. 4.3e+02;
Matches 79; Conservative 0; Mismatches 70; Indels 0; Gaps 0;
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DB 68666 GGCGCTGACGTCTGCTCCCGCGTGGAGACGCGGCGAGGACGCTTCGAGGACG 68607
QY 66 TCGAGTCGGCGCGCGCGACTCGACGATGACGAGATGACCACTCCGCGCGCACTCG 125
DB 68606 GCAGGGCGATGGCGCGCGCGGAGGACGAGTGGCGGAGGACGACGAGCGGACCG 68547
QY 126 ACGATGAGCGAGATGACCACTCCGCGCG 154
DB 68546 CCGCGCAGGAGAGAGCCCGCTCGGACG 68518

RESULT 29
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WPCOMMENT
Sequence split into 61 fragments LOCUS AP006618 Accession AP006618
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AP006618_02 200001 310000
AP006618_03 300001 410000
AP006618_04 400001 510000
AP006618_05 500001 610000
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AP006618_07 700001 810000
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AP006618_11 1100001 1210000
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Continuation (60 of 61) of AP006618 from base 5900001 (AP006618 Nocardia farcinica IFM 1
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Best Local Similarity 58.0%; Pred. No. 4.9e+02;
Matches 65; Conservative 0; Mismatches 47; Indels 0; Gaps 0;
QY 7 GAGCTGTCATCTCGCTCATCTGTCAGTGGCGCGGAGCTGTCATCTCGCTCATCGT 66
DB 18264 GGGCTCGGGCACTTCTCGTCGCCGACACGAGAGCCGCGCTGATCACCTCCGCGAGTA 18323
QY 67 CGAGTCGGCGCGCGCGCACTCGACGATGAGCGAGATGACCACTCCGCGCGC 118
DB 18324 CGCCTCGCGGTGACCGGGTGCACGCTGCGCGGCACTTCACCCGTCGCGGC 18375

RESULT 30
AP006618_59/c
WPCOMMENT

Sequence split into 61 fragments LOCUS AP006618 Accession AP006618

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AP006618_04	400001	510000
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AP006618_06	600001	710000
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AP006618_08	800001	910000
AP006618_09	900001	1010000
AP006618_10	1000001	1110000
AP006618_11	1100001	1210000
AP006618_12	1200001	1310000
AP006618_13	1300001	1410000
AP006618_14	1400001	1510000
AP006618_15	1500001	1610000
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AP006618_40	4000001	4110000
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Continuation (60 of 61) of AP006618 from base 5900001 (AP006618 Nocardia farcinica IFM 1

Query Match 23.9%; Score 36.8; DB 1; Length 110000;
Best Local Similarity 58.0%; Pred. No. 4.9e+02;
Matches 65; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

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DB 18375 GCGCCGAGCTGTCTATCTGCTCATCTGAGTCGCGCCGCGGACTCGACGATGAG 18316

QY 97 CGAGATGACCACTCCGCGCCGCGGACTCGACGATGACGATGACGATGACGATGAC 148
DB 18315 CGAGATGACCACTCCGCGCCGCGGACTCGACGATGACGATGACGATGACGATGAC 18264

RESULT 31
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WPCOMMENT

Sequence split into 26 fragments LOCUS AE016822 Accession AE016822

Fragment Name	Begin	End
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AE016822_02	200001	310000
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AE016822_04	400001	510000
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AE016822_16	1600001	1710000
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AE016822_21	2100001	2210000
AE016822_22	2200001	2310000
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AE016822_24	2400001	2510000
AE016822_25	2500001	2584158

Continuation (15 of 26) of AE016822 from base 1400001 (AE016822 Leifsonia xyli subsp. xy

Query Match 23.8%; Score 36.6; DB 1; Length 110000;
Best Local Similarity 68.0%; Pred. No. 5.4e+02;
Matches 51; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

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QY 66 TCGAGTCGCGCGCG 80
DB 73630 TCGAGTCGCGCGCG 73644

RESULT 32
AE016822_14/c
WPCOMMENT

Sequence split into 26 fragments LOCUS AE016822 Accession AE016822

Fragment Name	Begin	End
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AE016822_01	100001	210000
AE016822_02	200001	310000
AE016822_03	300001	410000
AE016822_04	400001	510000
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AE016822_06	600001	710000
AE016822_07	700001	810000
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AE016822_09	900001	1010000
AE016822_10	1000001	1110000
AE016822_11	1100001	1210000

AE016822_12	1200001	1310000
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AE016822_14	1400001	1510000
AE016822_15	1500001	1610000
AE016822_16	1600001	1710000
AE016822_17	1700001	1810000
AE016822_18	1800001	1910000
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AE016822_21	2100001	2210000
AE016822_22	2200001	2310000
AE016822_23	2300001	2410000
AE016822_24	2400001	2510000
AE016822_25	2500001	2584158
Continuation (15 of 26) of AE016822 from base 1400001 (AE016822 Leifsonia xyli subsp. xy		

Query Match 23.8%; Score 36.6; DB 1; Length 110000;
Best Local Similarity 68.0%; Pred. No. 5.4e+02;
Matches 51; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

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Db	73644	CGACCTCCTTCTCGATGACGCGCCAGCATCGACTGCGGCTGTTGACGATGAGC	73585
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RESULT 33
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LOCUS Rhodopseudomonas palustris CGA009 complete genome; segment 1/16.
ACCESSION BX572593 BX571963
VERSION BX572593.1 GI:39652705
KEYWORDS complete genomes.
SOURCE Rhodopseudomonas palustris CGA009
ORGANISM Rhodopseudomonas palustris CGA009
Rhodopseudomonas palustris CGA009
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Bradyrhizobiaceae; Rhodopseudomonas.
REFERENCE 1 (bases 1 to 349315)
AUTHORS Larimer,F.W., Chain,P., Hauser,L., Lamerdin,J., Malfatti,S., Do,L.,
Land,M.L., Pelletier,D.A., Beatty,J.T., Lang,A.S., Tabita,F.R.,
Gibson,J.L., Hanson,T.E., Bobst,C., Torres,J.L., Peres,C.,
Harrison,F.H., Gibson,J. and Harwood,C.S.
Complete genome sequence of the metabolically versatile
photosynthetic bacterium Rhodopseudomonas palustris
Nat. Biotechnol. 22 (1), 55-61 (2004)
JOURNAL 14704707
PUBMED 2 (bases 1 to 349315)
REFERENCE Larimer,F.W. and Harwood,C.S.
AUTHORS Rhodopseudomonas genome consortium
CONSTRM Direct Submission
TITLE Submitted (24-JUL-2003) Submitted on behalf of the Rhodopseudomonas
JOURNAL genome consortium, the DOE Joint Genome Institute, Production
Genomics Facility, 2800 Mitchell Drive, Walnut Creek, CA 94598,
USA, and the Genome Analysis Group, Oak Ridge National Laboratory,
1060 Commerce Park Drive, Oak Ridge, TN 37831, USA;
larimerf@ornl.gov
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CDS
23.8%; Score 36.6; DB 1; Length 349315;
Best local Similarity 58.9%; Pred. No. 4.3e+02;
Matches 63; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

Query Match
22 CTCATCGTCGAGTCGGCGCGCCGAGCTGTCATCTCGCTCATCTCGAGTCGGCGCCGC 81
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RESULT 34
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LOCUS Rhodopseudomonas palustris CGA009 complete genome; segment 1/16.
DEFINITION BX572593 BX571963
ACCESSION BX572593.1 GI:39652705
VERSION complete genomes.
KEYWORDS Rhodopseudomonas palustris CGA009
SOURCE Rhodopseudomonas palustris CGA009
ORGANISM Rhodopseudomonas palustris CGA009
Rhodopseudomonas palustris
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Bradyrhizobiaceae; Rhodopseudomonas.
1 (bases 1 to 349315)
Larimer,F.W., Chain,P., Hauser,L., Lamerdin,J., Malfatti,S., Do,L.,
Land,M.L., Pelletier,D.A., Beaty,J.T., Lang,A.S., Tabita,F.R.,
Gibson,J.L., Hanson,T.E., Bobst,C., Torres,J.L., Peres,C.,
Harrison,F.H., Gibson,J. and Harwood,C.S.
Complete genome sequence of the metabolically versatile
photosynthetic bacterium Rhodopseudomonas palustris
Nat. Biotechnol. 22 (1), 55-61 (2004)
14704707
2 (bases 1 to 349315)
Larimer,F.W. and Harwood,C.S.
Rhodopseudomonas genome consortium
Direct Submission
Submitted (24-JUL-2003) Submitted on behalf of the Rhodopseudomonas
genome consortium, the DOE Joint Genome Institute, Production
Genomics Facility, 2800 Mitchell Drive, Walnut Creek, CA 94598,
USA, and the Genome Analysis Group, Oak Ridge National Laboratory,
1060 Commerce Park Drive, Oak Ridge, TN 37831, USA;
larimerf@ornl.gov
location/Qualifiers
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Oy 87 CGACGATGACGAGATGACACGAGCTCGCGCGCGCGACTCGACGATGAG 133
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RESULT 35
AK063727 674 bp mRNA linear PLN 24-JUL-2003
LOCUS Oryza sativa (japonica cultivar-group) cDNA clone:001-120-E01, full
DEFINITION insert sequence.
ACCESSION AK063727.1 GI:32973745
VERSION AK063727.1
KEYWORDS FLI_CDNA; oligo-capping.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
1 The Rice Full-length cDNA Consortium, National Institute of
Agricultural Sciences Rice Full-length cDNA Project Team;
Kikuchi,S., Satoh,K., Nagata,T., Kawagashira,N., Doi,K.,
Kishimoto,N., Yazaki,J., Ishikawa,M., Yamada,H., Ooka,H., Hotta,I.,
Kojima,K., Namiki,T., Ohneda,E., Yahagi,W., Suzuki,K., Li,C.,
Ohtsuki,K., Shishiki,T., Foundation of Advancement of International
Science Genome Sequencing & Analysis Group; Ootomo,Y., Murakami,K.,
Iida,Y., Sugano,S., Fujimura,T., Suzuki,Y., Tsunoda,Y.,
Kurosaki,T., Kodama,T., Masuda,H., Kobayashi,M., Xie,Q., Lu,M.,
Narikawa,R., Sugiyama,A., Mizuno,K., Yokomizo,S., Nishikura,J.,
Ikeda,R., Ishibiki,J., Kawamata,M., Yoshimura,A., Miura,J.,
Kusumegi,T., Oka,M., Ryu,R., Ueda,M., Matsubara,K., RIKEN;
Kawai,J., Carninci,P., Adachi,J., Aizawa,K., Arakawa,T., Fukuda,S.,
Hara,A., Hashidume,W., Hayatsu,N., Imotani,K., Ishii,Y., Itoh,M.,
Kagawa,I., Kondo,S., Konno,H., Miyazaki,A., Osato,N., Ota,Y.,
Saito,R., Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T.,
Yoshino,M. and Hayashizaki,Y.
Collection, mapping, and annotation of over 28,000 cDNA clones from
japonica rice
Science 301 (5631), 376-379 (2003)

JOURNAL
MEDLINE 22752273
PUBMED 12869764
TITLE 2 (bases 1 to 674)
AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Doi,K.,
Fujimura,T., Fukuda,S., Hanagaki,T., Hara,A., Hashizume,W.,
Hayashida,K., Hayashizaki,Y., Hayatsu,N., Hiramoto,K., Hiraoka,T.,
Hori,F., Hotta,I., Iida,J., Iida,Y., Ikeda,R., Imamura,K.,
Imotani,K., Ishibiki,J., Ishii,Y., Ishikawa,M., Itoh,M., Kagawa,I.,
Kanagawa,S., Katoh,H., Kawagashira,N., Kawai,J., Kawamata,M.,
Kikuchi,S., Kishikawa-Hirozane,T., Kishimoto,N., Kobayashi,M.,
Kodama,T., Kojima,K., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
Koya,S., Kurihara,C., Kurosaki,T., Kusumegi,T., Li,C., Lu,M.,
Masuda,H., Matsubara,K., Matsuyama,T., Miura,J., Miyazaki,A.,
Mizuno,K., Murakami,K., Murata,M., Nagata,T., Nakamura,M.,
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Sakazume,N., Sano,H., Sasaki,D., Sato,K., Satoh,K., Shibata,K.,
Shinagawa,A., Shiraki,T., Shishiki,T., Sogabe,Y., Sugano,S.,
Sugiyama,A., Suzuki,K., Suzuki,Y., Tagami,M., Tagami-Takeda,Y.,
Tagawa,A., Takahashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A.,
Toya,T., Tsunoda,Y., Ueda,M., Waki,K., Xie,Q., Yahagi,W.,
Yamada,H., Yamamoto,M., Yasunishi,A., Yazaki,J., Yokomizo,S. and
Yoshimura,A.
Direct Submission
Submitted (05-DEC-2001) Shoshi Kikuchi, National Institute of
Agricultural Sciences, Department of Molecular Genetics, Head of
Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki
305-8602, Japan (E-mail:skikuchi@nias.affrc.go.jp,
Tel:81-29-838-7007, Fax:81-29-838-7007)
This clone is one of the 28k full-length cDNA clones from japonica
rice.
URL : http://cdna01.dna.affrc.go.jp/cDNA/
NIAS Rice Full-length cDNA Project Team: Kikuchi,S., Satoh,K.,
Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J.,
Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T.,
Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T. and
Yamamoto,M.
FAIS Genome Sequencing & Analysis Group: Ootomo,Y., Iida,Y.,
Fujimura,T., Ikeda,R., Ishibiki,J., Kawamata,M., Kobayashi,M.,
Kodama,T., Kurosaki,T., Kusumegi,T., Lu,M., Masuda,H., Miura,J.,
Mizuno,K., Narikawa,R., Nishikura,J., Oka,M., Ryu,R., Sugano,S.,
Sugiyama,A., Suzuki,Y., Tsunoda,Y., Ueda,M., Xie,Q., Yokomizo,S.,
Yoshimura,A., Matsubara,K. and Murakami,K.
Genome Exploration Research Group in Riken Genomic Sciences Center
and Genome Science Laboratory in Riken: Adachi,J., Aizawa,K.,
Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hanagaki,T.,
Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K.,
Hiraoka,T., Hori,F., Iida,J., Imamura,K., Imotani,K., Ishii,Y.,
Itoh,M., Kagawa,I., Kanagawa,S., Katoh,H., Kawai,J.,
Kishikawa-Hirozane,T., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,
Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Ohno,M., Osato,N.,
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Yasunishi,A. and Hayashizaki,Y.
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FEATURES
source

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Query Match 23.6%; Score 36.4; DB 8; Length 674;
Best Local Similarity 58.2%; Pred. No. 1.5e+03;
Matches 64; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

Oy 42 CGAGCTGTCATCTCGCTCATCTCGAGTCGCGCGCGCGCGACTCGACGATGACGAGA 101
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Oy 102 TGACCAGCTCCGCGCGCGACTCGACGATGAGCGAGTACCAGCTCCGG 151
Db 235 GCTTCGGGTTCGACTCGCGGTTTCGCGCGCGCGCGCGACGACCTCCGG 284

RESULT 36
AK063727/c 674 bp mRNA linear PLN 24-JUL-2003
LOCUS Oryza sativa (japonica cultivar-group) cDNA clone:001-120-E01, full
DEFINITION insert sequence.
ACCESSION AK063727
VERSION AK063727.1 GI:32973745
KEYWORDS FLI_CDNA; oligo-capping.
SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM

Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; *Oryza*.

REFERENCE
AUTHORS

1 The Rice Full-length cDNA Consortium, National Institute of
Agrobiological Sciences Rice Full-length cDNA Project Team;
Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K.,
Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I.,
Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C.,
Ohtsuki, K., Shishiki, T., Foundation of Advancement of International
Science Genome Sequencing & Analysis Group, Otsu, Y., Murakami, K.,
Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Tsunoda, Y.,
Kurosaki, T., Kodama, T., Masuda, H., Kobayashi, M., Xie, Q., Lu, M.,
Narikawa, R., Sugiyama, A., Mizuno, K., Yokomizo, S., Nishida, J.,
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Kawai, J., Carninci, P., Adachi, J., Aizawa, K., Arakawa, T., Fukuda, S.,
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Kagawa, I., Kondo, S., Konno, H., Miyazaki, A., Osato, N., Ota, Y.,
Saito, R., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T.,
Yoshino, M., and Hayashizaki, Y.

TITLE	Collection, mapping, and annotation of over 28,000 cDNA clones from japonica rice
JOURNAL	Science 301 (5631), 376-379 (2003)

PUBMED
REFERENCE
AUTHORS

2 (bases 1 to 674)
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Doi, K.,
Fujimura, T., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W.,
Hayashida, K., Hayashizaki, Y., Hayatsu, N., Hiramoto, K., Hirooka, T.,
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kodama, T., Kojima, K., Kojima, Y., Kondo, S., Komno, H., Kouda, M.,
Koya, S., Kurihara, C., Kurosaki, T., Kusumegi, T., Li, C., Lu, M.,
Masuda, H., Matsubara, K., Matsuyama, T., Miura, J., Miyazaki, A.,
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Namiki, T., Narikawa, R., Ninkura, J., Nishi, K., Nomura, K.,
Numasaki, R., Ohneda, E., Ohno, M., Ohtsuki, K., Oka, M., Ooka, H.,
Osato, N., Oca, Y., Otomo, Y., Ryu, R., Saitoh, H., Sakai, C., Sakai, K.,
Sakazume, N., Sano, H., Sasaki, D., Sato, K., Satoh, K., Shibata, K.,
Shinagawa, A., Shiraki, T., Shisniki, T., Sogabe, Y., Sugano, S.,
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Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A.,
Toya, T., Tsunoda, Y., Ueda, M., Waki, K., Xie, Q., Yahagi, W.,
Yamada, H., Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S. and
Yoshimura, A.

TITLE Direct Submission
JOURNAL Submitted (05-DEC-2001) Shoshi Kikuchi, National Institute of
Agrobiological Sciences, Department of Molecular Genetics, Head of
Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki
305-8602, Japan (E-mail: skikuchi@nias.affrc.go.jp,
Tel: 81-29-838-7007, Fax: 81-29-838-7007)

COMMENT

URL : <http://cdna01.dna.afrc.go.jp/cDNA/>
 NIAS Rice Full-length cDNA Project Team: Kikuchi, S., Satoh, K.,
 Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J.,
 Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T.,
 Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T. and
 Yamamoto, M.
 FAIS Genome Sequencing & Analysis Group: Otomo, Y., Iida, Y.,
 Fujimura, T., Ikeda, R., Ishibiki, J., Kawamata, M., Kobayashi, M.,
 Kodama, T., Kurosaki, T., Kusumegi, T., Lu, M., Masuda, H., Mura, J.,
 Mizuno, K., Narikawa, R., Nikura, J., Oka, M., Ryu, R., Sugano, S.,
 Sugiyama, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Xie, Q., Yokomizo, S.,
 Yoshimura, A., Matsubara, K. and Murakami, K.
 Genome Exploration Research Group in Riken Genomic Sciences Center
 and Genome Science Laboratory in Riken: Adachi, J., Aizawa, K.,
 Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hanagaki, T.,
 Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K.,

FEATURES

Hiraoka, T., Hori, F., Iida, J., Imamura, K., Imotani, K., Ishii, Y.,
 Itoch, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawai, J.,
 Kishikawa-Hirozane, T., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
 Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
 Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Ohno, M., Osato, N.,
 Ota, Y., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H.,
 Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T.,
 Sogabe, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F.,
 Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Waki, K.,
 Yasunishi, A. and Hayashizaki, Y.

Location/Qualifiers

1. .674

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/mol_type="mRNA"

/cultivar="Nipponbare"

/db_xref="taxon:39947"

/clone="001-120-E01"

ORIGIN

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Matches 64;	Conservative	0;	Mismatches 46;	Indels 0;
				Gaps 0

OY 4 CCGAGCTGGTCATCTCGCTCATGTCGAGTCCGCCGCCGAGCTGTGCATCTCGCTCAT 63
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Db 284 CCGAGGTCCTCGTCCGCCGCCGCCGAACCGCAGTCCGACC CGAAGCTGTTGCTCT 225

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QY      64 CGTCGAGTCGGCGGCGGCCGATCGATGAGCGAGATGACCAAGCTCCG 111
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RESULT 37	AC107207	LOCUS	DEFINITION	AC107207	133449 bp	DNA	linear	PLN 01-JAN-2000
			Oryza sativa chromosome 3 BAC OSJNB0106M04 genomic sequence, complete sequence.					
ACCESSION	AC107207							
VERSION	AC107207.9					GI:37514985		
KEYWORDS	HTG.							
SOURCE	Oryza sativa (japonica cultivar-group)							
ORGANISM	Oryza sativa (japonica cultivar-group)							

REFERENCE AUTHORS

REFERENCE	AUTHORS	TITLE	JOURNAL	REFERENCE
1 (bases 1 to 133449)	Buell, C.R., Yuan, Q., Ouyang, S., Liu, J., Gansberger, K., Jones, K.M., Overton II, L.L., Tsitirin, T., Kim, M.M., Bera, J.J., Jin, S.S., Fadrosch, D.W., Tallon, L.J., Koo, H., Zismann, V., Hsiao, J., Blunt, S., Vanaken, S.S., Riedmuller, S.B., Utterback, T.T., Feldblyum, T.V., Yang, Q.Q., Haas, B.J., Suh, B.B., Peterson, J.J., Quackenbush, J., White, O., Salzberg, S.L. and Fraser, C.M.	Oryza sativa chromosome 3 BAC OSJNB0106M04 genomic sequence	Unpublished	2 (bases 1 to 133449)

TITLE Direct Submission
JOURNAL Submitted (16-JAN-2002) The Institute for Genomic Research, 9712
Medical Center Dr, Rockville, MD 20850, USA
REFERENCE 3 (bases 1 to 133449)

TITLE	Direct Submission
JOURNAL	Submitted (28-SEP-2002) The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD 20850, USA
REFERENCE	4 (bases 1 to 133449)

AUTHORS Buell, R.
TITLE Direct Submission
JOURNAL Submitted (04-OCT-2003) The Institute for Genomic Research, 9712
Medical Center Dr, Rockville, MD 20850, USA
REFERENCE 5 (bases 1 to 133449)

REFERENCE	5 (bases 1 to 133449)
AUTHORS	Buell, R.
TITLE	Direct Submission
JOURNAL	Submitted (01-JAN-2004) The Institute for Genomic Research, 9712

Submitted (01-JAN-2004) The Institute for Genomic Research, 9712

COMMENT Medical Center Dr, Rockville, MD 20850, USA, rbuelli@tigr.org
On Oct 4, 2003 this sequence version replaced gi:23343713.
Address all correspondence to:rice@tigr.org

BAC clone OSJNB0106M04 is from *Oryza sativa* chromosome 3
The orientation of the sequence is from SP6 to T7 end of the BAC clone.
Genes were identified by a combination of several methods: Gene prediction programs including Fgenesh (<http://www.softberry.com/>), genscan and Genscan+ (Chris Burge, <http://CCR-081.mit.edu/GENSCAN.html>), GenemarkHM (Mark Borodovsky, <http://genemark.biology.gatech.edu/Genemark/>), and Geneslicer (Michaela Pertea and Steven Salzberg, contact mpertea@tigr.org), searches of the complete sequence against a peptide database and the plant EST database at TIGR (<http://www.tigr.org/tdb/cgi.shtml>). Annotated genes are named to indicate the level of evidence for their annotation. Genes with similarity to other proteins are named after the database hits. Genes without significant peptide similarity but with EST similarity are named as unknown proteins. Genes without protein or EST similarity, that are predicted by more than two gene prediction programs over most of their length are annotated as hypothetical proteins. Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, <http://genome.wustl.edu/eddy/tRNAscan-SE/>). Simple repeats are identified by repeatmasker (Arian Smit, <http://ftp.genome.washington.edu/RM/RepeatMasker.html>).

This BAC overlaps with rice BAC OSJNBa0079B15 (AC099043) and OSJNBa0072F13 (AC133450).

FEATURES
Source Location/Qualifiers

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/note="japonica cultivar-group"

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/note="predicted by fgenesh"

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337. .912

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LVAAIYASASTPGETSGPMKVNLIATGKGQKAI SNVVEFVSTAIVGVVDKTIHINT
VDQLFOGLTNASHDAKVELLVSCNGAVETWYKATHVMVSNANYSKSGSNGAGEG
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Best Local Similarity 58.2%; Pred. No. 5.7e+02;
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LOCUS Oryza sativa chromosome 3 BAC OSJNBa0072F13 genomic sequence,
DEFINITION complete sequence.
ACCESSION AC133450
VERSION AC133450.6 GI:45860990
KEYWORDS HTG.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
AUTHORS Buell,C.R., Yuan,Q., Ouyang,S., Liu,J., Gansberger,K., Jones,K.M.,
Overton II,J.L., Tsaltrin,T., Kim,M.M., Bera,J.J., Jin,S.S.,
Padrosh,D.W., Tallon,L.J., Koo,H., Zismann,V., Heiao,J., Blunt,S.,
Vanaken,S.S., Riedmuller,S.B., Utterback,T.T., Feldblyum,T.V.,
Yang,Q.Q., Haas,B.J., Suh,B.B., Peterson,J.J., Quackenbush,J.,
White,O., Salzberg,S.L. and Fraser,C.M.
Oryza sativa chromosome 3 BAC OSJNBa0072F13 genomic sequence
Unpublished
2 (bases 1 to 150743)
Buell,R.
Direct Submission
Submitted (12-SEP-2002) The Institute for Genomic Research, 9712
Medical Center Dr, Rockville, MD 20850, USA
3 (bases 1 to 150743)
Buell,R.
Direct Submission
Submitted (16-OCT-2003) The Institute for Genomic Research, 9712
Medical Center Dr, Rockville, MD 20850, USA
4 (bases 1 to 150743)
Buell,R.
Direct Submission
Submitted (31-MAR-2004) The Institute for Genomic Research, 9712
Medical Center Dr, Rockville, MD 20850, USA
5 (bases 1 to 150743)
Buell,R.
Direct Submission
Submitted (31-JUL-2004) The Institute for Genomic Research, 9712
Medical Center Dr, Rockville, MD 20850, USA, rbuelli@tigr.org
On Mar 31, 2004 this sequence version replaced gi:37693579.
Address all correspondence to:rice@tigr.org
BAC clone OSJNBa0072F13 is from Oryza sativa chromosome 3
The orientation of the sequence is from SP6 to T7 end of the BAC

clone.
Genes were identified by a combination of several methods: Gene prediction programs including Fgenesh (<http://www.softberry.com/>), genscan and Genscan+ (Chris Burge, <http://CCR-081.mit.edu/GENSCAN.html>), GenemarkHM (Mark Borodovsky, <http://genemark.biology.gatech.edu/Genemark/>), and Genesplicer (Michaela Pertea and Steven Salzberg, contact mpertea@tigr.org), searches of the complete sequence against a peptide database and the plant EST database at TIGR (<http://www.tigr.org/tdb/tgi.shtml>). Annotated genes are named to indicate the level of evidence for their annotation. Genes with similarity to other proteins are named after the database hits. Genes without significant peptide similarity but with EST similarity are named as unknown proteins. Genes without protein or EST similarity, that are predicted by more than two gene prediction programs over most of their length are annotated as hypothetical proteins. Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, <http://genome.wustl.edu/eddy/tRNAscan-SE/>). Simple repeats are identified by repeatmasker (Arian Smit, <http://ftp.genome.washington.edu/RM/RepeatMasker.html>).

This BAC overlaps with rice BAC OSJNB0106M04 (AC107207) and OSJNB0094003 (AC092781).

FEATURES
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CDS
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24815..24883
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mRNA

Query Match 23.6%; Score 36.4; DB 8; Length 150743; Best Local Similarity 58.2%; Pred. No. 5.5e+02; Matches 64; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

Qy 4 CCGAGCTGGTCATCTCGCTCATCTGAGTCGGCGCCGAGCTGTCATCTCGCTCAT 63 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| Db 117083 CCGAGGTCGTCGTCGGCGCCGCCGCAACCGGAGTCCGACCCGAGCTGTGCTCT 117142

Qy 64 CGTCGAGTCGGCGCGCCGCCGACTCGACATGAGCGAGATGACCACTCCG 113 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| Db 117143 CATCGAGCGCGCGCGAGACGCAACACCGGTAGCCGAACGCCG 117192

RESULT 40 AC133450/c 150743 bp DNA linear PLN 31-JUL-2004 LOCUS AC133450 Oryza sativa chromosome 3 BAC OSJNBa0072F13 genomic sequence, complete sequence. AC133450 AC133450.6 GI:45860990 HTG.

ACCESSION 150743 bp DNA linear PLN 31-JUL-2004 Oryza sativa (japonica cultivar-group) Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 150743) Buell,C.R., Yuan,Q., Ouyang,S., Liu,J., Gansberger,K., Jones,K.M., Overton II,L.L., Tsitrin,T., Kim,M.M., Bera,J.J., Jin,S.S., Fadrosch,D.W., Tallon,L.J., Koo,H., Zismann,V., Hsiao,J., Blunt,S., Vanaken,S.S., Riedmuller,S.B., Uterback,T.T., Feldlyum,T.V., Yang,Q.Q., Haas,B.J., Suh,B.B., Peterson,J.J., Quackenbush,J., White,O., Salzberg,S.L. and Fraser,C.M. Oryza sativa chromosome 3 BAC OSJNBa0072F13 genomic sequence Unpublished

2 (bases 1 to 150743) Buell,R. Direct Submission Submitted (12-SEP-2002) The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD 20850, USA

3 (bases 1 to 150743) Buell,R. Direct Submission Submitted (16-OCT-2003) The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD 20850, USA

4 (bases 1 to 150743) Buell,R. Direct Submission Submitted (31-MAR-2004) The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD 20850, USA

5 (bases 1 to 150743) Buell,R. Direct Submission Submitted (31-JUL-2004) The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD 20850, USA, rbuell@tigr.org On Mar 31, 2004 this sequence version replaced gi:37693579. Address all correspondence to:rice@tigr.org

REFERENCE AUTHORS JOURNAL TITLE JOURNAL

COMMENT BAC clone OSJNBa0072F13 is from Oryza sativa chromosome 3 The orientation of the sequence is from SP6 to T7 end of the BAC clone. Genes were identified by a combination of several methods: Gene prediction programs including fgenesh (<http://www.softberry.com/>),

genscan and Genscan+ (Chris Burge, <http://CCR-081.mit.edu/GENSCAN.html>), GeneMarkHM (Mark Borodovsky, <http://genemark.biology.gatech.edu/GeneMark/>), and Geneslicer (Mihaela Pertea and Steven Salzberg, contact mpertea@tigr.org), searches of the complete sequence against a peptide database and the plant EST database at TIGR (<http://www.tigr.org/tdb/cgi.shtml>). Annotated genes are named to indicate the level of evidence for their annotation. Genes with similarity to other proteins are named after the database hits. Genes without significant peptide similarity but with EST similarity are named as unknown proteins. Genes without protein or EST similarity, that are predicted by more than two gene prediction programs over most of their length are annotated as hypothetical proteins. Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, <http://genome.wustl.edu/eddy/tRNAscan-SE/>). Simple repeats are identified by repeatmasker (Arian Smit, <http://ftp.genome.washington.edu/RM/RepeatMasker.html>).

This BAC overlaps with rice BAC OSJNB0106M04 (AC107207) and OSJNB0094003 (AC092781).

FEATURES

source

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expression of the rice Kn1 type homeobox gene family
during embryo, shoot, and flower development(Plant Cell 11
(9), 1651 1664 (1999)); contains Pfam profile PF03790:
KNOX1 domain and PF03791: KNOX2 domain; EST cDNA AK107296
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(Gene 326, 13 22 (2004)); contains Pfam profile PF00249:
Myb like DNA binding domain; EST cDNA AK112018 from this
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Best local Similarity 58.2%; Pred. No. 5.5e+02;
Matches 64; Conservative 0; Mismatches 46; Indels 0; Gaps 0;
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RESULT 41
AY081837
LOCUS
DEFINITION
AY081837 8973 bp DNA linear BCT 20-APR-2002
Bradyrhizobium japonicum isolate PM200P9-2 putative amidase Amic
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2-dehydro-3-deoxyphosphogalactonate aldolase (dgoA),
2-dehydro-3-deoxygalactonate kinase (dgoK), putative alkanal
monooxygenase (luxA2), HpaC (hpaC), and sigma 54 activator (acor)
genes, complete cds; and unknown genes.
AY081837
AY081837.1 GI:20257158
Bradyrhizobium japonicum
Bradyrhizobium japonicum
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Bradyrhizobiaceae; Bradyrhizobium.
1 (sites)
Mueller, P.
tnxpk2 insertions in the Bradyrhizobium japonicum poxB gene
(pyruvate dehydrogenase) affect the symbiotic interaction within
soybean nodules
Unpublished
2 (bases 1 to 8973)
Mueller, P.
Direct Submission
Submitted (04-MAR-2002) Biology, Cell Biology and Applied Botany,
Philips University Marburg, Karl-von-Frisch-Str., Marburg 35032,
Germany
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ORIGIN
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Matches 59; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

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Oy   100 GATGACCAGCTCCGCGCCGCGACTCGACGATGACGA 136
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DEFINITION  Bradyrhizobium japonicum isolate pPM200P9-2 putative amidase Amic
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            monoxygenase (luxA2), HpaC (hpaC), and sigma 54 activator (acOR)
            genes, complete cds; and unknown genes.
ACCESSION   AY081837
VERSION     AY081837.1   GI:20257158
KEYWORDS

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SOURCE ORGANISM	REFERENCE AUTHORS TITLE	JOURNAL	REFERENCE AUTHORS TITLE	JOURNAL
Bradyrhizobium japonicum	Bradyrhizobium japonicum	Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Bradyrhizobiaceae; Bradyrhizobium.	1 (sites)	Unpublished
Bradyrhizobium japonicum	tnkPK2 insertions in the Bradyrhizobium japonicum poxB gene (pyruvate dehydrogenase) affect the symbiotic interaction within soybean nodules	Unpublished	2 (bases 1 to 8973)	Unpublished
Bradyrhizobium japonicum	Mueller, P.	Submitted (04-MAR-2002) Biology, Cell Biology and Applied Botany, Philipps University Marburg, Karl-von-Frisch-Str., Marburg 35032, Germany	Direct Submission	Submitted (04-MAR-2002) Biology, Cell Biology and Applied Botany, Philipps University Marburg, Karl-von-Frisch-Str., Marburg 35032, Germany
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gene	Bradyrhizobium japonicum	/gene="amiC"	<1. .1079	/gene="amiC"
CDS	Bradyrhizobium japonicum	/codon_start=3	/transl_table=11	/product="putative amidase AmiC"
gene	Bradyrhizobium japonicum	/protein_id="AA12345.1"	/db_xref="GI:20257160"	/translation="AARPTIRPSTSRALPGTADYTCGSSAGSAAVAAGVPIAHATDGGGIRIPAGVNGNIGLKVSRGVSLAHPMSDLTGLVSIQCGQSRSVRDTAFVDHARGPARGEMFPWTTAHPISEMIKDPGLKRIALSHTWGYTATPEIAAELEKTRFLEGLGHVDVYALPELDERAAFEQTCWYISNFAVVISNMLAARGLDKDPEDLIEPMNIRIWEAGRHTSPAERAKMQGVNNTSRGFGAFPEQWDVILPTLALPTPKVGTRVYLTISDNPDLDFGMLMRFEFTPLANLGMFAISMPMATQDHDLPLGIQAIKQANDGLLIQLAAQIERALDGMNGRKKPKVHVS"
CDS	Bradyrhizobium japonicum	1586. .2179	/note="ORF197; conserved hypothetical protein"	/codon_start=1
gene	Bradyrhizobium japonicum	/transl_table=11	/product="unknown"	/protein_id="AA12350.1"
CDS	Bradyrhizobium japonicum	/db_xref="GI:20257165"	/translation="MSSSSTSGLPATLPFEBLAETKGRSDYGHISGLQDLRFAPAEAMSSLPYRPVFGVDTETGVLHGVTAMLDSCGMAYQALDGTATATDLRIDYOKPATPGDLIDIKAHSVCYRTTRSLAFVSTAYQESSEDPVATATACFMIGANRTMLADRRWIRAHPPDGGAGGSGWPVRPQPVRALPRHPRQRTAR"	2110. .2508
gene	Bradyrhizobium japonicum	/note="ORF132"	/codon_start=1	/transl_table=11
CDS	Bradyrhizobium japonicum	/product="unknown"	/protein_id="AA12349.1"	/db_xref="GI:20257164"
gene	Bradyrhizobium japonicum	/translation="MARSPARSRAASASASTTGTLLTLPSPKTIIGQSDPARDPWRH	DRLLPRDHGDHGRTRARRRRAPQADRADHQLALRRARQLCQCLDRQAGPRIVAFERAGRIMTSSRSRSPNCFGHMLRPTPNDEE"	2579. .2842
gene	Bradyrhizobium japonicum	/note="ORF87"	/codon_start=1	/transl_table=11
CDS	Bradyrhizobium japonicum	/product="unknown"	/protein_id="AA12351.1"	/db_xref="GI:20257166"
gene	Bradyrhizobium japonicum	/translation="MRHPSGSSPMFGRHVAAMRSWVDATPKELTAVLIAIGA	VVITAVFYYPGCPRTDFAVFAALWLISDIAIAFISPKECRIS"	complement (2945. .4654)
gene	Bradyrhizobium japonicum	/gene="poxB"	complement (2945. .4654)	/gene="poxB"
CDS	Bradyrhizobium japonicum	complement (2945. .4654)	/gene="poxB"	

gene
CDS

/codon_start=1
/transl_table=1
/product="pyruvate dehydrogenase"
/protein_id="AAI12352.1"
/db_xref="GI:20257167"

translation="MAINNVADLFVATLEQAGVKRIYGIVGDSLNAFTALRRGTTIE
WIRHREEVAAFAAAGEAQMTGSILAVCGSCGPENGLINGLFDARSRVRPVLIAAQ
IPSAEIGGGYFQETHPNQLFRECHYCELVSDASQLPFIENAIRAVGLRGVAVIAM
PGDVAFRDPERRALSTARGLALSAPKVPPEANELKALDDLNGAERTLLFCRGCAGA
HAPLMOLAELKSPIVHALGGKEHEYENPYDVGMTGFIGSSGYAAMHACDALVMLG
TDFPYKQFFPTGCCIQIIDIRPENLGRQADHRGRSAAEDQDPAQAYSTMPSRITRR
RARGWTRSPGAPPGSKPIHPQYLAKVSDHASEDA VETADVGTPTVMARYLEMNGRR
RLIGSFVHGSMANAMPQAIGAQSQGRQVISLSGDGFTMLMGDLITLTOMKL PVKY
VVENNGLVFVALEMKAAGFVDTNVDLQNPDFAAMARAMGI FAKRVDPGELPGA VKE
MLAHNGRALLDVVTAKQELSMPTITTEQIKGFSLWVLRAVMNRRGGRCARCLAKTNL
LPR"

complement(4735. .5367)
/gene="dgoA"
complement(4735. .5367)
/gene="dgoA"
/note="putative KHG/KDPG aldolase"
/codon_start=1
/transl_table=1
/product="2-dehydro-3-deoxyphosphogalactonate aldolase"
/protein_id="AAI12353.1"
/db_xref="GI:20257168"

translation="MSVPFPSPMKRPVLAILRGVKEEAESIVSVLIEAGMTAIDPLN
SPDPFSRIATAKLAPAAVLIGAGTVLTTADVDRLNDVGGKLMVSPNVDQVLARAHO
YAMVTLPGVFSPTREALLAARSAGSLKFPPASVLSAGSITAIRAVLPAGVMTAAVGV
SDONFAEYIKGVTAFLGSSLYKPGMSAADVAARAKQTIAAYDRAIVKD"
complement(5383. .6288)
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complement(5383. .6288)
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/codon_start=1
/transl_table=1
/product="2-dehydro-3-deoxygalactonate kinase"
/protein_id="AAI12346.1"
/db_xref="GI:20257161"

translation="MSYVAVDWGTSSFRWLVDRAQVLAERRSGEGMILAAKTGFAG
VLQSHSAVEAPDHLPLYVCMAAGAKTGWEAGYVDTAPLTSILKQPVPEGEARDI
RLPGIAQRDAGAPDVMRGEETQLLGALGLKAGAEALVCMPTGHSKWVRVKDGTVEHF
STFMTELFSVISRDITLSLAVA GADDAEDVASFKAAVKAAFEAPAFANULLEGARS
QLLEFGSTA AARETISGTLIGABLAGLSGNVTKGITLVA SGRLATTLYQLAFDELVS
TPRLVDADAEAVRHGLSMAAAIWTS"

gene
CDS

6521. .7618
/gene="luxA2"
6521. .7618
/gene="luxA2"
/codon_start=1
/transl_table=1
/product="putative alkanal monooxygenase"
/protein_id="AAI12348.1"
/db_xref="GI:20257163"

translation="MEIGYFTMPSHRPECGLKEGNDWDLOVMRWLDELGYQEAWVGEH
HTAPWEPNPTDLLIAOLMOTKRLRIGPGFLLPYHPAPELANRYAMLDMSEGRLN
FGYAASGLPSDMAMENVDMGSGQNRDMTREALEII LKMWTDPAPWTYKGKFWTVTKPD
TMEDFLKPHIKPLQAPHPENRVAGLSKNSDTLKLAGERGFI PMSLINNPAYVGSHMWS
VEIGAAGTKRKPNRQDWLRVREVFADTDEBAWKLISTGDMGRMMHEYFLPLLGHFGF
KDYLIKHADVPDRHVTV EYCAKRNIWGSPATVAEKIEKIYDEVGRCVLLVFGFDYK
HKAEAWHSLSLSSSEVMRLKHLGSARKAA"

gene
CDS

7615. .8229
/gene="hpac"
7615. .8229
/gene="hpac"
/codon_start=1
/transl_table=1
/product="hpac"
/protein_id="AAI12347.1"
/db_xref="GI:20257162"

translation="MTRRGCGAIVPHPPRRSPREVDAKOFKQMRQCAGAVALT
GAHGKRTGLTVTSACSLSDNPSSLIVCNRNASAHTRIREGAFPAINFLHEDHALLA
LTESGOKGVNGDNDRFAEGOWTRPAGTAGAPUTDAVAFDCI AOEFTKTHSI FVGEV
P

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gene      GVSHSDGAPLVYLRSSFVHPHEIRGTVSVDLSRHLSTWDFS"
           complement(8407. .8973)
           /gene="acor"
           complement(8407. .8973)
CDS       /gene="acor"
           /codon_start=1
           /transl_table=11
           /product="sigma 54 activator"
           /db_xref="GI:20257159"
           /translation="MOTRLRLVLENREVMPLGALKPVPVDIRLISATHRDLGRMAEEG
AFRADLYPRLRGMEVVKLPSLRERADDDIROIAREEAPNCRLSDRAWLLSAYPYPG
NMRQLRHVLRLAGCTAENGVTVDADLDPLFGRAADGPRGGRARDDRGAQAQAMRSC
VPRARALKLSRATLVRIKIKIKIETAQ"

ORIGIN
Query Match      23.5%; Score 36.2; DB 1; Length 8973;
Best Local Similarity 60.8%; Pred. No.1e+03;
Matches 59; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

QY 19 TCGCTCATCGTCGAGTCGCGCGCGAGCTGTCATCTCGCTCATCGTCGAGTCGCGCGC 78
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 5359 TCCCTTCCGTCGATGAGCGCTCCGCTGTCGCGATCCTCGCGCGGCGTCAAGCCGAGGA 5300
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 79 CGCCGACTCGACGATGAGCGGAGATGACCACTCCCGC 115
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 5299 GGGCGAGTCATCGTCAGCGTGTCTGATCGAGCGCGC 5263
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 43
LOCUS      AC008771      123169 bp      DNA      linear      PRI 28-FEB-2001
DEFINITION Homo sapiens chromosome 5 clone CTD-2015H6, complete sequence.
ACCESSION  AC008771
VERSION     AC008771.4   GI:13162500
KEYWORDS    HTG.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 123169)
AUTHORS    DOE Joint Genome Institute and Stanford Human Genome Center.
TITLE      Direct Submission
JOURNAL    Unpublished
REFERENCE   2 (bases 1 to 123169)
AUTHORS    DOE Joint Genome Institute.
TITLE      Direct Submission
JOURNAL    Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint
            Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
REFERENCE   3 (bases 1 to 123169)
AUTHORS    DOE Joint Genome Institute and Stanford Human Genome Center.
TITLE      Direct Submission
JOURNAL    Submitted (28-FEB-2001) DOE Joint Genome Institute, 2800 Mitchell
            Drive, Walnut Creek, CA 94598, USA
COMMENT     On Feb 28, 2001 this sequence version replaced gi:7709299.
            Draft Sequence Produced by DOE Joint Genome Institute
            www.jgi.doe.gov
            Finishing Completed at Stanford Human Genome Center
            www.shgc.stanford.edu
            Quality: Phrap Quality >=40 99.3% of Sequence;
            Estimated Total Number of Errors is 0.9.
            STS Content:
            SHGC-84992 G53847
            WI-15051 G23648
            WI-17790 G24283.
FEATURES
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                1..123169
                /organism="Homo sapiens"
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                /db_xref="taxon:9606"
                /chromosome="5"
                /clone="CTD-2015H6"
ORIGIN
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Query Match      23.5%; Score 36.2; DB 9; Length 123169;
Best Local Similarity 55.0%; Pred. No.6.3e+02;
Matches 71; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

QY 20 CGCTCATCGTCGAGTCGCGCGCGGAGCTGTGTCATCTCGCTCATCTGTCGAGTCGCGCGC 79
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 94608 CGGCGCTCGTCACCATGCGACGATCCGCTGAGGCCAGGTAAAGCCGAGCGCGCGCC 94667
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 80 GCCGACTCGACGATGAGCGGAGATGACCACTCCGCGCGCGGAGCTCGACGATGAGCGAGAT 139
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 94668 TCTGCTCGAGGTGGGCGCTTTGAGAGGCTCCGCGCGCGGTACCTCCCTTGGCGGGCT 94727
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 140 GACCAGCTC 148
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 94728 CCCGCGGTC 94736
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 44
LOCUS      AC008771/c      123169 bp      DNA      linear      PRI 28-FEB-2001
DEFINITION Homo sapiens chromosome 5 clone CTD-2015H6, complete sequence.
ACCESSION  AC008771
VERSION     AC008771.4   GI:13162500
KEYWORDS    HTG.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 123169)
AUTHORS    DOE Joint Genome Institute and Stanford Human Genome Center.
TITLE      Direct Submission
JOURNAL    Unpublished
REFERENCE   2 (bases 1 to 123169)
AUTHORS    DOE Joint Genome Institute.
TITLE      Direct Submission
JOURNAL    Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint
            Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
REFERENCE   3 (bases 1 to 123169)
AUTHORS    DOE Joint Genome Institute and Stanford Human Genome Center.
TITLE      Direct Submission
JOURNAL    Submitted (28-FEB-2001) DOE Joint Genome Institute, 2800 Mitchell
            Drive, Walnut Creek, CA 94598, USA
COMMENT     On Feb 28, 2001 this sequence version replaced gi:7709299.
            Draft Sequence Produced by DOE Joint Genome Institute
            www.jgi.doe.gov
            Finishing Completed at Stanford Human Genome Center
            www.shgc.stanford.edu
            Quality: Phrap Quality >=40 99.3% of Sequence;
            Estimated Total Number of Errors is 0.9.
            STS Content:
            SHGC-84992 G53847
            WI-15051 G23648
            WI-17790 G24283.
FEATURES
    source      location/Qualifiers
                1..123169
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                /mol_type="genomic DNA"
                /db_xref="taxon:9606"
                /chromosome="5"
                /clone="CTD-2015H6"
ORIGIN
Query Match      23.5%; Score 36.2; DB 9; Length 123169;
Best Local Similarity 55.0%; Pred. No.6.3e+02;
Matches 71; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

QY 7 GAGCTGTCATCTCGCTCATCTCGAGTCGCGCGCGGAGAGCTGTGTCATCTCGCTCATCGT 66
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 94736 GACCGCGGAGAGCCCGCAAGGAGAGGTACGCGCGCGGAGGCTCTCAAGCGCCCACT 94677
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 67 CGAGTCGCGCGCGCGGACTGACGATGAGCGGAGATGACCACTCCGCGCGCGGAGCTCGA 126
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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Db 94676 CCAGGACAGAGCCCGCGCTCGCGCTTACCTGGGCTCCAGCGATGCTGCATGTGA 94617
QY 127 CGATGAGCG 135
Db 94616 CGACGCCCG 94608

RESULT 45
AC018764 126052 bp DNA linear PRI 13-MAR-2003
LOCUS Homo sapiens chromosome 5 clone CTD-2327L5, complete sequence.
DEFINITION AC018764
ACCESSION AC018764
VERSION AC018764.8 GI:28933541
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 126052)
DOE Joint Genome Institute and Stanford Human Genome Center.
Direct Submission
Unpublished

REFERENCE

2 (bases 1 to 126052)
DOE Joint Genome Institute.

REFERENCE

Submitted (19-DEC-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
3 (bases 1 to 126052)
DOE Joint Genome Institute and Stanford Human Genome Center.

REFERENCE

Submitted (01-JUL-2000) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
4 (bases 1 to 126052)
DOE Joint Genome Institute and Stanford Human Genome Center.

REFERENCE

Submitted (09-NOV-2000) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
5 (bases 1 to 126052)
DOE Joint Genome Institute and Stanford Human Genome Center.

REFERENCE

Submitted (30-JAN-2003) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
6 (bases 1 to 126052)
DOE Joint Genome Institute and Stanford Human Genome Center.

REFERENCE

Submitted (13-MAR-2003) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
On Mar 13, 2003 this sequence version replaced gi:28144392.
Draft Sequence Produced by DOE Joint Genome Institute

REFERENCE

Submitted (13-MAR-2003) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
On Mar 13, 2003 this sequence version replaced gi:28144392.
Draft Sequence Produced by DOE Joint Genome Institute

REFERENCE

Submitted (13-MAR-2003) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
On Mar 13, 2003 this sequence version replaced gi:28144392.
Draft Sequence Produced by DOE Joint Genome Institute

REFERENCE

Submitted (13-MAR-2003) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
On Mar 13, 2003 this sequence version replaced gi:28144392.
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Drive, Walnut Creek, CA 94598, USA
On Mar 13, 2003 this sequence version replaced gi:28144392.
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REFERENCE

Submitted (13-MAR-2003) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
On Mar 13, 2003 this sequence version replaced gi:28144392.
Draft Sequence Produced by DOE Joint Genome Institute

REFERENCE

Submitted (13-MAR-2003) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
On Mar 13, 2003 this sequence version replaced gi:28144392.
Draft Sequence Produced by DOE Joint Genome Institute

REFERENCE

Submitted (13-MAR-2003) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
On Mar 13, 2003 this sequence version replaced gi:28144392.
Draft Sequence Produced by DOE Joint Genome Institute

REFERENCE

Submitted (13-MAR-2003) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
On Mar 13, 2003 this sequence version replaced gi:28144392.
Draft Sequence Produced by DOE Joint Genome Institute

Db 86887 CCAGGACAGAGCCCGCGCTCGCGCTTACCTGGGCTCCAGCGATGCTGCATGTGA 86946
QY 127 CGATGAGCG 135
Db 86947 CGACGCCCG 86955

Search completed: April 8, 2005, 23:58:42
Job time : 1897 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 8, 2005, 23:09:54 ; Search time 132 Seconds
(without alignments)
1908.990 Million cell updates/sec

Title: US-09-887-194A-13
Perfect score: 154
Sequence: 1 cgccgcgagctggtcattc.....gagatgaccagctccgcg 154

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Issued Patents NA: *
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq: *
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3: /cgn2_6/ptodata/1/ina/6A_COMB.seq: *
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq: *
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq: *
6: /cgn2_6/ptodata/1/ina/backfile1.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34.8	22.6	1681	3 US-09-434-288-7	Sequence 7, Appli
2	34.8	22.6	1681	3 US-09-434-288-7	Sequence 7, Appli
3	34	22.1	4403765	3 US-09-103-840A-2	Sequence 2, Appli
4	34	22.1	4403765	3 US-09-103-840A-2	Sequence 2, Appli
5	34	22.1	4411529	3 US-09-103-840A-1	Sequence 1, Appli
6	34	22.1	4411529	3 US-09-103-840A-1	Sequence 1, Appli
7	33.4	21.7	747	4 US-09-252-991A-4417	Sequence 4417, Ap
8	33.4	21.7	747	4 US-09-252-991A-4417	Sequence 4417, Ap
9	33.4	21.7	3225	4 US-09-252-991A-4622	Sequence 4622, Ap
10	33.4	21.7	3225	4 US-09-252-991A-4622	Sequence 4622, Ap
11	33	21.4	345	4 US-09-513-999C-8640	Sequence 8640, Ap
12	33	21.4	345	4 US-09-513-999C-8640	Sequence 8640, Ap
13	32.4	21.0	1110	4 US-09-902-540-2360	Sequence 2360, Ap
14	32.4	21.0	1110	4 US-09-902-540-2360	Sequence 2360, Ap
15	32.4	21.0	2238	1 US-07-841-651-1	Sequence 1, Appli
16	32.4	21.0	2238	1 US-07-841-651-1	Sequence 1, Appli
17	32.4	21.0	15447	4 US-09-902-540-1100	Sequence 1100, Ap
18	32.4	21.0	15447	4 US-09-902-540-1100	Sequence 1100, Ap
19	32.2	20.9	579	4 US-09-252-991A-8862	Sequence 8862, Ap
20	32.2	20.9	579	4 US-09-252-991A-8862	Sequence 8862, Ap
21	32.2	20.9	807	4 US-09-252-991A-15671	Sequence 15671, A
22	32.2	20.9	807	4 US-09-252-991A-15671	Sequence 15671, A
23	32.2	20.9	876	4 US-09-252-991A-8753	Sequence 8753, Ap
24	32.2	20.9	876	4 US-09-252-991A-8753	Sequence 8753, Ap
25	32.2	20.9	1203	4 US-09-252-991A-15578	Sequence 15578, A
26	32.2	20.9	1203	4 US-09-252-991A-15578	Sequence 15578, A
27	32.2	20.9	1869	4 US-09-252-991A-15737	Sequence 15737, A

C 28	32.2	20.9	1869	4 US-09-252-991A-15737	Sequence 15737, A
C 29	32.2	20.9	1899	4 US-09-252-991A-8973	Sequence 8973, Ap
C 30	32.2	20.9	1899	4 US-09-252-991A-8973	Sequence 8973, Ap
C 31	32	20.8	921	4 US-09-902-540-3748	Sequence 3748, Ap
C 32	32	20.8	921	4 US-09-902-540-3748	Sequence 3748, Ap
C 33	32	20.8	1093	4 US-09-902-540-7905	Sequence 7905, Ap
C 34	32	20.8	1093	4 US-09-902-540-7905	Sequence 7905, Ap
C 35	32	20.8	2119	3 US-09-032-372-6	Sequence 6, Appli
C 36	32	20.8	2119	3 US-09-032-372-6	Sequence 6, Appli
C 37	32	20.8	7994	4 US-09-902-540-797	Sequence 797, App
C 38	32	20.8	7994	4 US-09-902-540-797	Sequence 797, App
C 39	32	20.8	17897	4 US-09-902-540-1182	Sequence 1182, Ap
C 40	32	20.8	17897	4 US-09-902-540-1182	Sequence 1182, Ap
C 41	31.6	20.5	2496	4 US-09-252-991A-13526	Sequence 13526, A
C 42	31.6	20.5	2496	4 US-09-252-991A-13526	Sequence 13526, A
C 43	31.6	20.5	2622	4 US-09-252-991A-13933	Sequence 13933, A
C 44	31.6	20.5	2622	4 US-09-252-991A-13933	Sequence 13933, A
C 45	31.6	20.5	2685	4 US-09-252-991A-13826	Sequence 13826, A
C 46	31.6	20.5	2685	4 US-09-252-991A-13826	Sequence 13826, A
C 47	31.6	20.5	34094	4 US-09-292-034-1	Sequence 1, Appli
C 48	31.6	20.5	34094	4 US-09-292-034-1	Sequence 1, Appli
C 49	31.4	20.4	1125	4 US-09-902-540-2467	Sequence 2467, Ap
C 50	31.4	20.4	1125	4 US-09-902-540-2467	Sequence 2467, Ap
C 51	31.4	20.4	1242	4 US-09-489-039A-3619	Sequence 3619, Ap
C 52	31.4	20.4	1242	4 US-09-489-039A-3619	Sequence 3619, Ap
C 53	31.4	20.4	1404	4 US-09-902-540-3484	Sequence 3484, Ap
C 54	31.4	20.4	1404	4 US-09-902-540-3484	Sequence 3484, Ap
C 55	31.4	20.4	1707	4 US-09-266-965-68	Sequence 68, Appli
C 56	31.4	20.4	1707	4 US-09-266-965-68	Sequence 68, Appli
C 57	31.4	20.4	2069	4 US-09-949-016-3309	Sequence 3309, Ap
C 58	31.4	20.4	2069	4 US-09-949-016-3309	Sequence 3309, Ap
C 59	31.4	20.4	2148	4 US-09-489-039A-3539	Sequence 3539, Ap
C 60	31.4	20.4	2148	4 US-09-489-039A-3539	Sequence 3539, Ap
C 61	31.4	20.4	3202	4 US-09-949-016-1127	Sequence 1127, Ap
C 62	31.4	20.4	3202	4 US-09-949-016-1127	Sequence 1127, Ap
C 63	31.4	20.4	14077	4 US-09-902-540-1109	Sequence 1109, Ap
C 64	31.4	20.4	14077	4 US-09-902-540-1109	Sequence 1109, Ap
C 65	31.4	20.4	17188	4 US-09-902-540-1166	Sequence 1166, Ap
C 66	31.4	20.4	17188	4 US-09-902-540-1166	Sequence 1166, Ap
C 67	31.4	20.4	53500	4 US-09-266-965-76	Sequence 76, Appli
C 68	31.4	20.4	53500	4 US-09-266-965-76	Sequence 76, Appli
C 69	31.4	20.4	135667	4 US-09-949-016-15051	Sequence 15051, A
C 70	31.4	20.4	135667	4 US-09-949-016-15051	Sequence 15051, A
C 71	31	20.1	2562	4 US-09-489-039A-5900	Sequence 5900, Ap
C 72	31	20.1	2562	4 US-09-489-039A-5900	Sequence 5900, Ap
C 73	30.8	20.0	2079	4 US-09-252-991A-3097	Sequence 3097, Ap
C 74	30.8	20.0	2079	4 US-09-252-991A-3097	Sequence 3097, Ap
C 75	30.8	20.0	2787	3 US-09-105-537-40	Sequence 40, Appli
C 76	30.8	20.0	2787	3 US-09-105-537-40	Sequence 40, Appli
C 77	30.8	20.0	5970	3 US-09-320-878-21	Sequence 21, Appli
C 78	30.8	20.0	5970	3 US-09-320-878-21	Sequence 21, Appli
C 79	30.8	20.0	5970	4 US-09-141-908-11	Sequence 11, Appli
C 80	30.8	20.0	5970	4 US-09-141-908-11	Sequence 11, Appli
C 81	30.8	20.0	5970	4 US-09-141-908-11	Sequence 21, Appli
C 82	30.8	20.0	5970	4 US-09-141-908-11	Sequence 21, Appli
C 83	30.6	19.9	1734	6 5352575-8	Patent No. 5352575
C 84	30.6	19.9	1734	6 5352575-8	Patent No. 5352575
C 85	30.6	19.9	1734	6 5352575-8	Patent No. 5352575
C 86	30.6	19.9	1734	6 5352575-8	Patent No. 5352575
C 87	30.6	19.9	3114	4 US-09-902-540-2501	Sequence 2501, Ap
C 88	30.6	19.9	3114	4 US-09-902-540-2501	Sequence 2501, Ap
C 89	30.6	19.9	16833	4 US-09-902-540-1112	Sequence 1112, Ap
C 90	30.6	19.9	16833	4 US-09-902-540-1112	Sequence 1112, Ap
C 91	30.4	19.7	480	4 US-09-902-540-8058	Sequence 8058, Ap
C 92	30.4	19.7	480	4 US-09-902-540-8058	Sequence 8058, Ap
C 93	30.4	19.7	1881	4 US-09-252-991A-4030	Sequence 4030, Ap
C 94	30.4	19.7	1881	4 US-09-252-991A-4030	Sequence 4030, Ap
C 95	30.4	19.7	7160	4 US-09-902-540-821	Sequence 821, App
C 96	30.4	19.7	7160	4 US-09-902-540-821	Sequence 821, App
C 97	30.4	19.7	8563	4 US-09-902-540-3318	Sequence 3318, Ap
C 98	30.4	19.7	8563	4 US-09-902-540-3318	Sequence 3318, Ap
C 99	30.4	19.7	8604	4 US-09-902-540-5331	Sequence 5331, Ap
C 100	30.4	19.7	8604	4 US-09-902-540-5331	Sequence 5331, Ap

Db 4251891 GCGTTGAGATGATCACCACGCCACCGACTGGCCGGAATACGGCGGTACGGCTGCGC 4251832
Qy 97 CGAGATGACCACTCCGGCCCGACTCGACGATGAGC 134
Db 4251831 CGGGGTGTCCAGCTTCGGCTTCGGCGCGCCCAACGCGC 4251794

RESULT 5

US-09-103-840A-1
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: 24366-2007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1

Query Match 22.1%; Score 34; DB 3; Length 4411529;
Best Local Similarity 59.2%; Pred. No. 10;
Matches 58; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

Qy 21 GCTCATCGTGAAGTCGCGCGCCGAGCTGTCATCTGCTCATCTGAGTCGGCGCGC 80
Db 4259538 GCGCGTTGGCGCGCCGAGAGCTGACACCCCGCCAGCGGTAGCCGCGTATC 4259597
Qy 81 CCGACTGACGATGAGCGAGATGACCACTCCGCGCGC 118
Db 4259598 GCGGCCAGTCGGTGGCGGTGATCATCTTCAACCGC 4259635

RESULT 6

US-09-103-840A-1/c
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: 24366-2007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1

Query Match 22.1%; Score 34; DB 3; Length 4411529;
Best Local Similarity 59.2%; Pred. No. 10;
Matches 58; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

Qy 37 GCGGCCGAGTGTATCTGCTCATCTGAGTCGGCGCGCCGACTCGACGATGAG 96
Db 4259635 GCGGTGAAGATGATCACACGCGCCGCACTGGCCGGAATACGGCGGTACGCGCTGCGC 4259576

Qy 97 CGAGATGACCACTCCGGCCCGACTCGACGATGAGC 134
Db 4259575 CGGGGTGTCCAGCTTCGGCTTCGGCGCGCCCAACGCGC 4259538

RESULT 7

US-09-252-991A-4417
; Sequence 4417, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 4417
; LENGTH: 747
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-4417

Query Match 21.7%; Score 33.4; DB 4; Length 747;
Best Local Similarity 58.6%; Pred. No. 9.8;
Matches 58; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

Qy 24 CATCTGAGTCCGGCGCCGAGCTGTCATCTGCTCATCTGAGTCGGCGCGCGC 83
Db 420 CATCTGACAGAGAGCGCGGAGCGGCTGCGCAGCCGAGCAATGCGGTGCGCA 479
Qy 84 ACTGACGATGAGCGAGATGACCACTCCGCGCGCGAC 122
Db 480 ACTGTCGATGCGCGCCAGAGCTTGGTGGCGGTGAC 518

RESULT 8

US-09-252-991A-4417/c
; Sequence 4417, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 4417
; LENGTH: 747
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-4417

Query Match 21.7%; Score 33.4; DB 4; Length 747;
Best Local Similarity 57.0%; Pred. No. 9.8;
Matches 61; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

Qy 33 GTCGGCGCCGAGTGTATCTGCTCATCTGAGTCGGCGCGCCGACTCGACGA 92
Db 518 GTCAGCGCCGACGAGGCTTCGGCGCGCATGACGAGTTGGGACCGGCAATCCGTCCG 459
Qy 93 TGAGCGATGACCAAGTCCGCGCGCGACTCGACGATGACGAGAT 139

Db 458 GCTGCCACCGCCGCTCGCCGCTCTGCTGCCAGATGTCATCAT 412

RESULT 9

US-09-252-991A-4622
; Sequence 4622, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 4622
; LENGTH: 3225
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-4622

Query Match

21.7%; Score 33.4; DB 4; Length 3225;
Best Local Similarity 58.6%; Pred. No. 11;
Matches 58; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

QY 24 CATCGTCAGTCGCGCCGCGAGCTGTCATCTGCTCATCTGAGTCGGCGCGCG 83

Db 16 CATCTGGCAGCAGAGAGCGCGCGCAGCGCGCTGGCGCAGCCGCGAGCAATGCCGCTGCCA 75

QY 84 ACTCGACGATGAGCGGAGATGACCAAGCTCCGCGCGCGCGAC 122

Db 76 ACTGCTCGATGCGCGCGCAGAGCCTGCTGCGCGCGCTGAC 114

RESULT 10

US-09-252-991A-4622/C
; Sequence 4622, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 4622
; LENGTH: 3225
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-4622

Query Match 21.7%; Score 33.4; DB 4; Length 3225;
Best Local Similarity 57.0%; Pred. No. 11;
Matches 61; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

QY 33 GTCGCGCGCGAGCTGTCATCTGCTCATCTGTCGAGTCGGCGCGCGCGCGACTGCAGCA 92

Db 114 GTCAGCGCGCGCAGCAGGCTCTGCGCGCGCATCGAGCAGTTGGCGACCGCGCATTCGTCG 55

QY 93 TGAGCGAGATGACCAAGCTCCGCGCGCGCGACTCGACGATGAGCGAGAT 139

Db 54 GCTGCCACCGCGCGCTCGCGCGCTCTGCTGCCAGATGTCATCAT 8

RESULT 11

US-09-513-999C-8640
; Sequence 8640, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 8640
; LENGTH: 345
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 73
; OTHER INFORMATION: n=a, g, c or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 319
; OTHER INFORMATION: y=c or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 320
; OTHER INFORMATION: k=g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 321
; OTHER INFORMATION: y=c or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 336
; OTHER INFORMATION: k=g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 345
; OTHER INFORMATION: m=a or c
US-09-513-999C-8640

Query Match

21.4%; Score 33; DB 4; Length 345;
Best Local Similarity 62.3%; Pred. No. 12;
Matches 48; Conservative 2; Mismatches 27; Indels 0; Gaps 0;

QY 3 GCCGAGCTGTCATCTGCTCATCTGTCGAGTCGGCGCGCGAGCTGTCATCTGCTCA 62

Db 246 GCCCGACGTGTCATTTCTCTCACCACCGAGCCTACCGCGCGAGTGTCTTCCCTCA 305

QY 63 TCGTCGAGTCGGCGCC 79

Db 306 CCACCGAGCCTACCYKC 322

RESULT 12

US-09-513-999C-8640/C
; Sequence 8640, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24

; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 1100
; LENGTH: 15447
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-1100

Query Match 21.0%; Score 32.4; DB 4; Length 15447;
Best Local Similarity 60.0%; Pred. No. 20;
Matches 54; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

QY 49 GGTGATCTGCTCATGTCGAGTCGGCGCCCGCCGACTCGACGATGAGCGAGATGACCAAG 108
DB 4671 GGTGCGCGCGCGACCTTCGCGTCCACGCGCGAGCGAGCGCATGTGTGGCAAGGGCACTC 4612

QY 109 CTCCGCGCGCGACTCGACGATGAGCGAGA 138
DB 4611 CTTCGCGCGCGCATCGCGTGAGCATGA 4582

RESULT 19

US-09-252-991A-8862
; Sequence 8862, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 8862
; LENGTH: 579
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-8862

Query Match 20.9%; Score 32.2; DB 4; Length 579;
Best Local Similarity 57.4%; Pred. No. 19;
Matches 58; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

QY 53 ATCTGCTCATGTCGAGTCGGCGCCCGACTCGACGATGAGCGAGATGACCACTCC 112
DB 280 ACCCGACCTCAACGAGTATGCTGCGCCCGCAAGCCGATCGCCGAGCGACCATCAC 339

QY 113 GCGCGCGACTCGACGATGAGCGAGATGACCACTCCGCC 153
DB 340 ATCGCGCGCAAGCGCCGAGGGCAAGCGGCAATCATGCC 380

RESULT 20

US-09-252-991A-8862/c
; Sequence 8862, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 8862

; LENGTH: 579
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-8862

Query Match 20.9%; Score 32.2; DB 4; Length 579;
Best Local Similarity 57.4%; Pred. No. 19;
Matches 58; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

QY 2 GCGCGAGCTGTGATCTGCTCATGTCGAGTCGGCGCCCGAGCTGTCATCTGCTC 61
DB 380 GCGATGATCTGCCCTTGCTCGCGCGCGGCGGCGATGTGATGTGCTCGCG 321

QY 62 ATCGTGAAGTCGGCGCGCGCGACTCGACGATGAGCGAGAT 102
DB 320 ATCGGCTTGCCGCGCAGCAATACTCGTTGAGGGTGGGGT 280

RESULT 21

US-09-252-991A-15671
; Sequence 15671, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 15671
; LENGTH: 807
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-15671

Query Match 20.9%; Score 32.2; DB 4; Length 807;
Best Local Similarity 57.4%; Pred. No. 20;
Matches 58; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

QY 54 TCTGCTCATGTCGAGTCGGCGCCCGCGACTCGACGATGAGCGAGATGACCACTCCG 113
DB 521 TCGAGCGCATCTGCGGATGCTCGCGCCACCTCGCCGAGGGCTACGCGCACTGCG 580

QY 114 GCGCGCGACTCGACGATGAGCGAGATGACCACTCCGCC 154
DB 581 CTGCGTGAAGCGAGCGCGGATTTCCGAGAGCTCGGGCTG 621

RESULT 22

US-09-252-991A-15671/c
; Sequence 15671, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 15671
; LENGTH: 807
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa

Db 1819 ATCGCTTGCCGCGCAGCAACTACTGTTGAGGTCGGGT 1779

RESULT 31

US-09-902-540-3748
; Sequence 3748, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 3748
; LENGTH: 921
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-3748

Query Match 20.8%; Score 32; DB 4; Length 921;
Best Local Similarity 62.5%; Pred. No. 22;
Matches 50; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 48 TGGTCATCTCGTCATCGTGCAGTCGGCGCGCCGACTCGACGATGAGCGAGATGACCA 107
DB 782 TGGGCATCTCCACCGCGCGCGCTGTCCGCGTGAATCAGAGCTGGCGAGATGACCG 841
QY 108 GCTCCGCGCGCGCGCTGAC 127
DB 842 ACGGCAGCGCGCTGCTGCC 861

RESULT 32

US-09-902-540-3748/c
; Sequence 3748, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 3748
; LENGTH: 921
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-3748

Query Match 20.8%; Score 32; DB 4; Length 921;
Best Local Similarity 62.5%; Pred. No. 22;
Matches 50; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 28 GTGAGTGGCGCGCGAGCTGTGATCTCGTCATCTGAGTCGGCGCGCCGACTC 87
DB 861 GCGAGCAGCGCGCTGCCGTGCTATCTGCCAGCTTCTGATTACGGCGACAGCGC 802
QY 88 GACGATGAGCGAGATGACCA 107
DB 801 GCGCGCGGTGAGATGCCCA 782

RESULT 33

US-09-902-540-7905
; Sequence 7905, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 7905
; LENGTH: 1093
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-7905

Query Match 20.8%; Score 32; DB 4; Length 1093;
Best Local Similarity 53.1%; Pred. No. 22;
Matches 68; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 27 CGTCAGTCGGCGCGGAGCTGTGATCTCGCTCATCTGAGTCGGCGCGCGACT 86
DB 281 CGCTGGCGCTTCCAGAGCTGAGCGGTCACTCACCGGCTGGCGCAGCGCTGTCG 340
QY 87 CGACATGAGCGAGATGACCACTCCGCGCGCACTCGACGATGAGCGAGATGACCA 146
DB 341 CCGCGAGGCGGAGCGGAGCGCGCCCACTTCCCTGCACACGGCGCTGTCGACGAGC 400
QY 147 TCCGCGCG 154
DB 401 TGACGCGG 408

RESULT 34

US-09-902-540-7905/c
; Sequence 7905, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 7905
; LENGTH: 1093
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-7905

Query Match 20.8%; Score 32; DB 4; Length 1093;
Best Local Similarity 53.1%; Pred. No. 22;
Matches 68; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 1 CCGCGGAGCTGTGATCTCGCTCATCTGAGTCGGCGCGCGAGCTGTGATCTGCT 60
DB 408 CCGGTGAGCTGTGAGAGCGCGCTGTGAGGCGAGGTGGCGGCTCCGCTTCCG 349
QY 61 CATGTCAGTCGGCGCGCGCACTCGACGATGAGCGAGATGACCACTCCGCGCGCG 120
DB 348 CTCGCGCGGAGCAGCGCGCTGCGCCAGCCGCTGAGCTGACCGCTCAGCTCCTGCA 289

QY 121 ACTGACG 128
DB 288 CCGCAGCG 281

RESULT 35

US-09-032-372-6
; Sequence 6, Application US/09032372
; Patent No. 6008337
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Yue, Henry
; APPLICANT: Lal, Preeti
; TITLE OF INVENTION: CELL CYCLE RELATED PROTEINS
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/032,372
; FILING DATE: Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0478 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2119 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: SYNORAB01
; CLONE: 78191
; US-09-032-372-6

Query Match 20.8%; Score 32; DB 3; Length 2119;

Best Local Similarity 51.4%; Pred. No. 23;
Matches 74; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

QY 5 CGAGCTGTCATCTCGCTCATCGTCGAGCTGGCGCGCCGAGCTGTCATCTCGCTCATC 64
DB 151 CGAGGCTCTCCGCTTCCCTCTCCGCTGCGTCCCGCGCGAAGATGGCAACCGAGGGGCTG 210
QY 65 GTCGAGTCGGCGCGCCGCGACTCGACATGAGCGAGATGACCGAGCTCCGGCGCGGACTC 124
DB 211 CACGAGACGAGACGCTGCGCTGAGAGAGCGAGGCCGAGAGCTCTCAAGGGCAAGCTG 270
QY 125 GACGATGAGCGAGATGACCGAGCTC 148
DB 271 GAGGAGAGCGAGCCCAAGCTGCAC 294

RESULT 36

US-09-032-372-6/c
; Sequence 6, Application US/09032372
; Patent No. 6008337
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Yue, Henry
; APPLICANT: Lal, Preeti
; TITLE OF INVENTION: CELL CYCLE RELATED PROTEINS
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/032,372
; FILING DATE: Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0478 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2119 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: SYNORAB01
; CLONE: 78191
; US-09-032-372-6

Query Match 20.8%; Score 32; DB 3; Length 2119;

Best Local Similarity 51.4%; Pred. No. 23;
Matches 74; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

QY 7 GAGCTGTCATCTCGCTCATCGTCGAGCTGGCGCGCCGAGCTGTCATCTCGCTCATCT 66
DB 294 GTGAGCTTGCTGCTGCTCTCTCTCAAGCTTGCCCTTGAGGCTCTCGGCTGCTTCA 235
QY 67 CGAGTCGGCGCGCCGCGACTCGACATGAGCGAGATGACCGAGCTCCGGCGCGGACTCGA 126
DB 234 CGAGCGCAGCTCTCGTCTCTGTCAGCCCTCGGTTGTCATCTTCCGCGGAGCGCAG 175
QY 127 CGATGAGCGAGATGACCGAGCTCCG 150
DB 174 CGAGAGGGAAGCGAGAGGCTCG 151

RESULT 37

US-09-902-540-797
; Sequence 797, Application US/0902540
; Patent No. 6833447
; GENERAL INFORMATION:

```

; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 797
; LENGTH: 7994
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-797
```

```

Query Match      20.8%; Score 32; DB 4; Length 7994;
Best Local Similarity 53.1%; Pred. No. 25;
Matches 68; Conservative 0; Mismatches 60; Indels 0; Gaps 0;
```

```

QY 27 CGTCGAGTCGGCGCGCGGCTGTCATCTCGCTCATCTGTCGAGTCGGCGCGCGGCGGACT 86
DB 6302 CGCTCGCGCGCTTCGACGAGCTGAGCGGTCAGCTCACCAGGCTGGCGCAGCGCGCTGTCG 6361
QY 87 CGACGATGAGCGAGATGACCACTCCGCGCGCGGCTGACGATGAGCGAGATGACCACTG 146
DB 6362 CGCGCGAGGCGGAGCGGCGCGCGCGGCTGCGCTGACACAGCGCGCTGTCGACGAGC 6421
QY 147 TCCGCGCGG 154
DB 6422 TGACGCGG 6429
```

RESULT 38

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US-09-902-540-797/c
; Sequence 797, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 797
; LENGTH: 7994
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-797
```

```

Query Match      20.8%; Score 32; DB 4; Length 7994;
Best Local Similarity 53.1%; Pred. No. 25;
Matches 68; Conservative 0; Mismatches 60; Indels 0; Gaps 0;
```

```

QY 1 CGGCGGAGCTGGTCATCTCGCTCATCTGAGTCGGCGCGGAGCTGTCATCTCGCT 60
DB 6429 CCGCGTCAGCTCGTCGACAGCGCGCGGTGTCAGAGGCTGGCGCGGCTTCGCTTCCG 6370
QY 61 CATCGTCAGTCGGCGCGCGGCTGACGATGAGCGGAGATGACCACTTCGCGCGCGG 120
DB 6369 CTCCGCGCGCAGCAGCGCGCTGCGCGCGGCTGAGCTGACCGCTCAGCTCTCGGACG 6310
QY 121 ACTCGACG 128
DB 6309 CCGCAGCG 6302
```

```

RESULT 39
US-09-902-540-1182
; Sequence 1182, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 1182
; LENGTH: 17897
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(17897)
; OTHER INFORMATION: unsure at all n locations
US-09-902-540-1182
```

```

Query Match      20.8%; Score 32; DB 4; Length 17897;
Best Local Similarity 62.5%; Pred. No. 25;
Matches 50; Conservative 0; Mismatches 30; Indels 0; Gaps 0;
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```

QY 48 TGGTCATCTCGCTCATCTGTCGAGTCGGCGCGCGGCTGACGATGAGCGAGATGACCA 107
DB 13389 TGGCATCTCCACCGCGCGCGCTGTCGCGCTGAATCAGAAGCTGGCGGAGATGACCG 13448
QY 108 GCTCGCGCGCGCGGCTGAC 127
DB 13449 ACGCAGCGCGCTGCTCGCC 13468
```

RESULT 40

```

US-09-902-540-1182/c
; Sequence 1182, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 1182
; LENGTH: 17897
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(17897)
; OTHER INFORMATION: unsure at all n locations
US-09-902-540-1182
```

```

Query Match      20.8%; Score 32; DB 4; Length 17897;
Best Local Similarity 62.5%; Pred. No. 25;
Matches 50; Conservative 0; Mismatches 30; Indels 0; Gaps 0;
```

```

QY 28 GTCGAGTCGGCGCGGAGCTGTCATCTCGCTCATCTGAGTCGGCGCGGCGGCGGACTC 87
DB 13468 GCGGAGCAGCGGCTGCGCTGTCATCTCGCGCAGCTTGAATTACGCGGAGACGCGC 13409
```


US-09-252-991A-13826
; Sequence 13826, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 13826
; LENGTH: 2685
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-13826

Query Match 20.5%; Score 31.6; DB 4; Length 2685;
Best Local Similarity 62.8%; Pred. No. 29;
Matches 49; Conservative 0; Mismatches 29; Indels 0; Gaps 0;
QY 43 GGAGCTGTCATCTCGCTCATCGTCGAGTCGGCGCGCCGCGGACTCGACGATGAGCGAGAT 102
Db 1576 GGAACAGATCCCTGATCAGCACCGTCGGCGCGCGCCGCGGACTCAAGCCGAAGAGCGAGAA 1635
QY 103 GACCAGCTCCGGCGCGCG 120
Db 1636 GGCCATCTGCGGCTGCAG 1653

Search completed: April 9, 2005, 00:55:08
Job time : 154 secs